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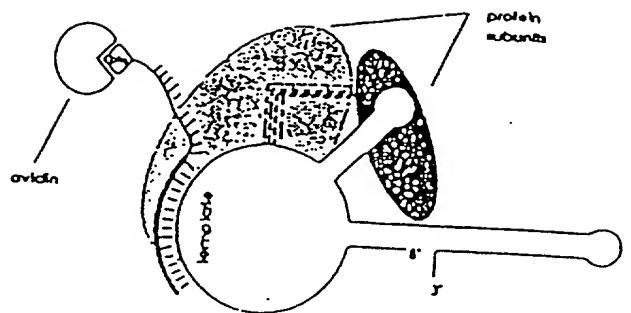
In re: Cech et al.

Application No.: To be assigned

Filed: January 18, 2002

For: NOVEL TELOMERASE

PANEL A



PANEL B

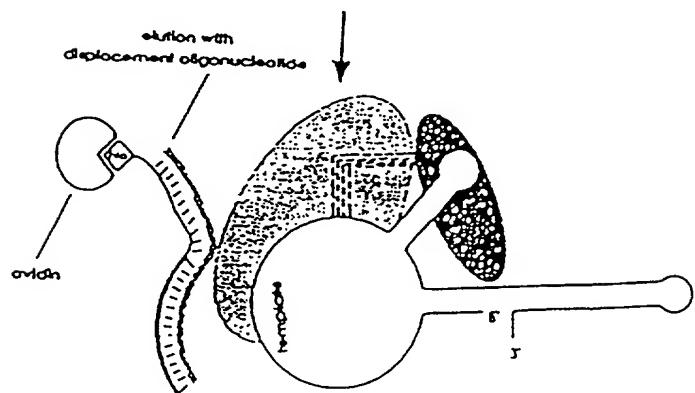


FIGURE 2

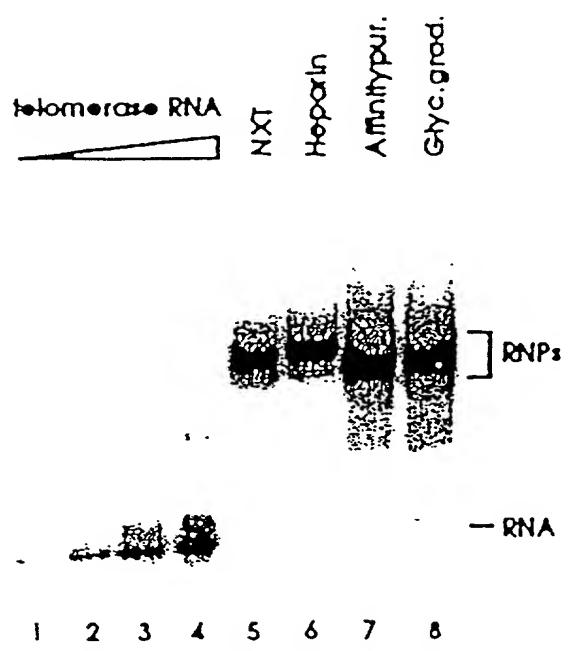


FIGURE 3

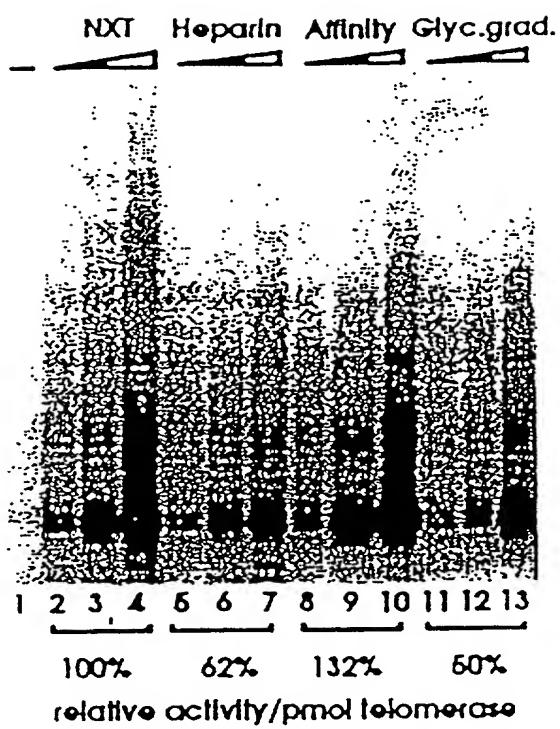


FIGURE 4

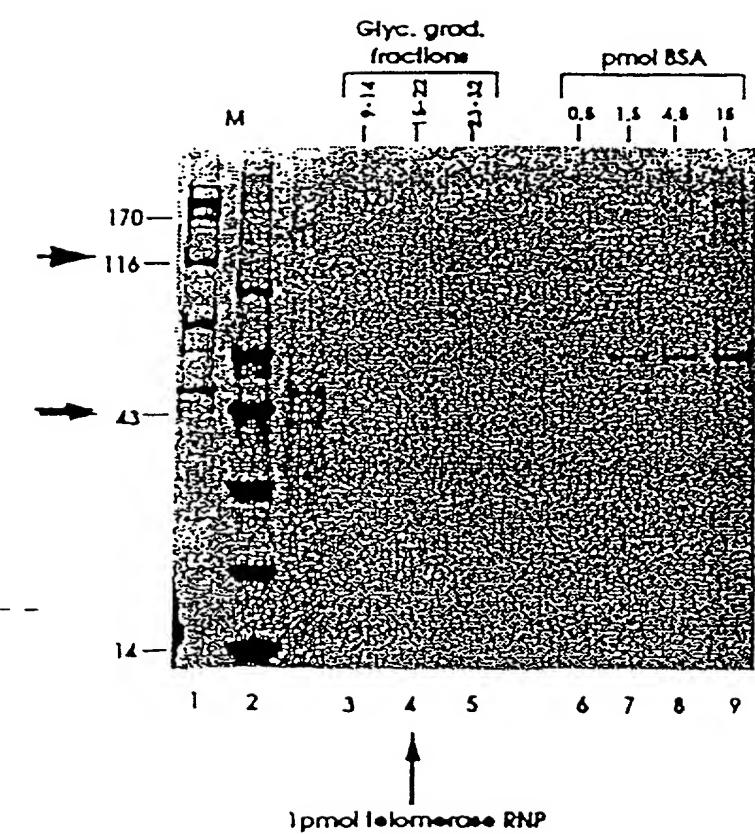


FIGURE 5

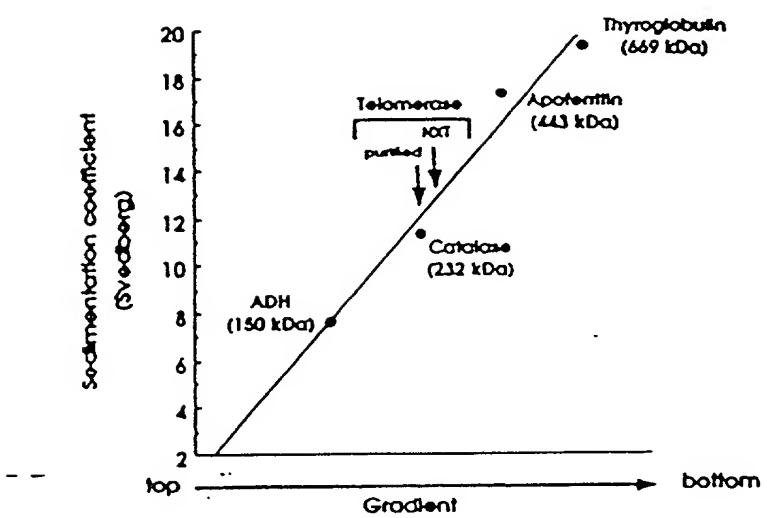


FIGURE 6

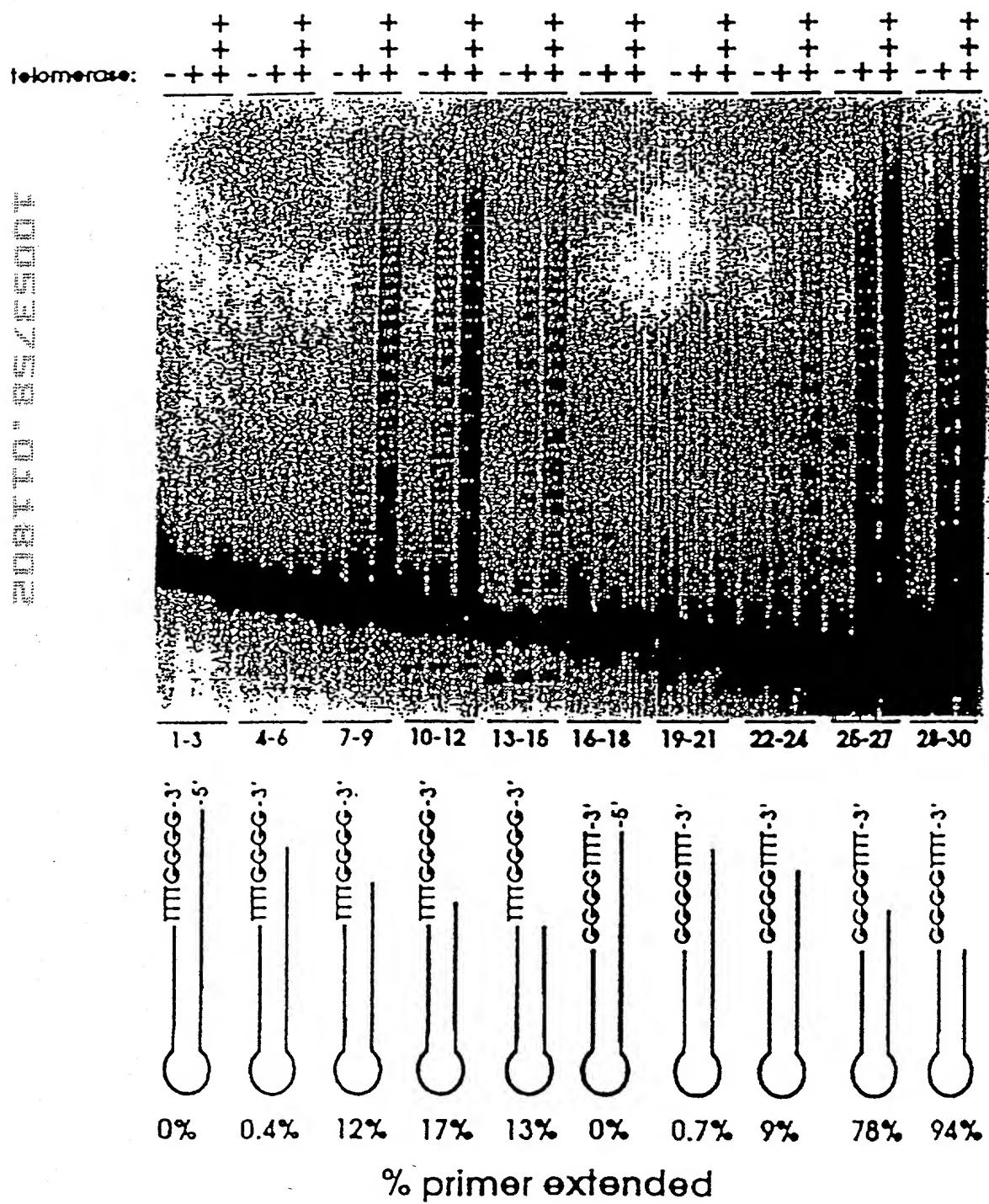
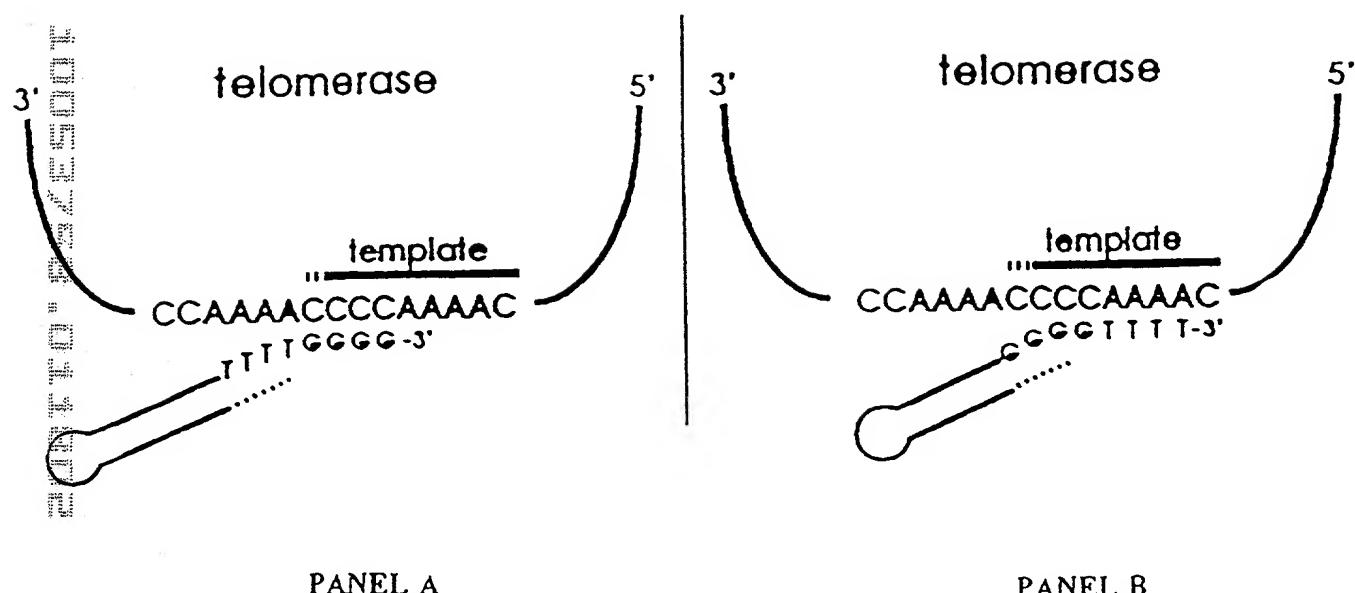
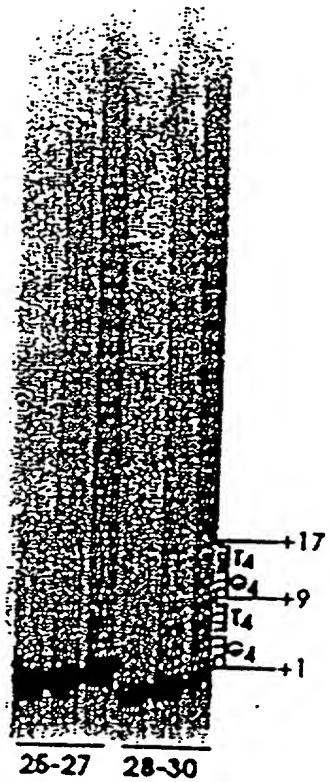


FIGURE 7



## FIGURE 8



### FIGURE 9

1 AAAACCCCAA AACCCCCAAA CCCCTTTAG AGCCCTGCAG TTGGAAATAT  
51 AACCTCAGTA TTAATAAGCT CAGATTAA ATATTAATTAA CAAAACCTAA  
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC  
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAC TAAAACGTIG TACTCTTGGAA  
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCAT TTATAAAGAT  
251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG  
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT  
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT  
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTITCA  
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAAACA GCTCTTCAA  
501 CTCAAAAGCA GTATTTCTT CAAGACGAAT GGAACCAAGT TAGAGCAATG  
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA  
601 GCGAACTTCT GAAGGAACCTC TTGTTCAATT TTGCGGGAAAT AACGTTTTG  
651 ATCATTGAA AGTCAACGAT AAGTTGACA AAAAGAAAAA AGGTGGAGCA  
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
751 GAATGAGAAA GATCACTTTC TCAACAAACAT CAACGTGCCG AATTGGAATA  
801 ATATGAAATC AAGAACCGAG ATATTTATT GCACTCATT TAATAGAAAT  
851 ACCAATTCT TCAAAAAGCA TGAGTTGTG AGTAACAAAAA ACAATATTTC  
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTTC AGATTAAATA  
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAAT TGCCTACATG  
1001 CTTGAGAAAG TCAAAGATT TAACTTCAAC TACTATTAA CAAAATCTG  
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA  
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC  
1151 TACACAACTG ATAATAAAATG CGTCACACAA TTTATTAAATG AATTITTC  
1201 CAATATACTC CCCAAAGACT TTTGACTGG AAGAAACCGT AAGAATTTC  
1251 AAAAGAAAGT TAAGAAATAT GTGGAACCTAA ACAAGCATGA ACTCATT  
1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA  
1351 GGTTGAGACC TCTGCAAAGC ATTITTTATT TTTGATCAC GAAAACATCT  
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGCTCG  
1451 CTGATTAGAT GATTITCTA TGTCAACCGAG CAACAGAAAAA GTTACTCCAA  
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA  
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT  
1601 GAAGAATGGA AAAAGTCGCT TGGATTGCA CCTGGAAAAC TCAGACTAAT  
1651 ACCGAAGAAA ACTACTTCC GTCCAATTAT GACTTCAAT AAGAAGATTG  
1701 TAAATTCAAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG  
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC  
1801 TTTGGATTG GCTGTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG  
1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTGCA  
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC  
1951 AACATTCTA AAAACTACTA AATTACTTTC TTCAAGATTTC TGGATTATGA  
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTGCAAAAC  
2051 TTTAGAAAGA AAGAAATGAA AGATTATTT AGACAGAAAT TCCAGAAGAT  
2101 TGCACITGAA GGAGGACAAT ATCCAACCTT ATTCAAGTGTGTT CTTGAAAATG  
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA  
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCAT TTAATATTG  
2251 CCAATATAAT TACATTAAC TTAATGGGA GTTTTATAAA CAAACAAAAG  
2301 GAATTCCCTCA AGGTCTTGA GTTTCATCAA TTTGTCATC ATTITATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATT CTTAGAGATG AATCAATGAA  
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTITAT TGAGAAACTT  
2501 ATAAACGTAA GTCGTAAAAA TGGATTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC  
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT  
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT  
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC  
2801 CATTATTTA GAAAGACGAT TACAACCGAA GACTTGCAG ATAAAACCTCT  
2851 CAACAAGTTA TTATATTCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG  
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC  
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
3001 CCTTGTGTGC AATATTAAGG ATACAATT TTGGAGAGGAG CATTATCCAG  
3051 ACTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAAA  
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAA  
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTGGA AAGTTAATT TCAATTGGT TCTTATATAC  
3251 TGGGGTTTG GGGTTTGGG GTTTGGGG

## FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQQVIRC RNQSQSHYKD  
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
101 SSSDVSDRQK LQCFGQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA  
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTTR IFYCTHFNRN  
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM  
301 LEKVKDFNPN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH  
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS  
451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV  
501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL  
551 NSHMLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN  
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ  
701 RNYFKKDNLQ QPVINICQYN YINFNGKFYK QTGKIPQGLC VSSILSSFYY  
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL  
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
851 SIDMKTALM PNINLRIEGI LCTLNLMQT KKASMWLKKK LKSFLMNNT  
901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID  
951 LEVSKIYISV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK  
1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

## FIGURE 11

1 CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAAGA AAAAATTGAG  
51 GTAGTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA  
101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA  
151 GCTCTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA  
201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT  
251 CTCGGATGCA AATCTTATA ACGATTCTT CTTGAGAAAA TTAGTTTAA  
301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTAAATAA  
351 AATCAGGTAA TGAGGATTAT TCTATTTTT AGATCACTTC TTAAGGAGCA  
401 TTATGGAGAA ATTACTTAA TACTAAAAGG TAAACAGTT GGATTATTTC  
451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG  
501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG  
551 AAAAAGTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTG  
601 TATGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC  
651 TTGAGACAAT TGAAAAAGCT GTTTACAAC GAAGGAATCG CAGTTCTGAA  
701 AGTTCTGATG TGTATGCCAT TATTITGTGA ATTAATCTCA AATATCTTAT  
751 CTCATTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT  
801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTATA  
851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTAGC  
901 TTACAACAGA TTACCTGTT TGATTACTCT TGCTCATCTC TTATATCTT  
951 AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTICAAAAT  
1001 TTGTTGATT TCCTGTAACC GGAATTAAACA ACAAGAATAT TAGCAACGAA  
1051 AAAGAAGAAG AGCTATCACA ATCCTGATT TCATAAGATT CAAAAATTCC  
1101 AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTCATT  
1151 CACAGCTGTT ATTTCTTT ATCTTAACAA TATTITGA TTAGCTGGAA  
1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT  
1251 TCACATTCA AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA  
1301 GCAGTCATCC GTTTAAAAA TAGTGCTATG AGGACTAAAT TTTAGAGTC  
1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA  
1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG  
1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAA  
1501 GTAACTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG  
1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAA  
1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA  
1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA  
1701 AAGATTATT TTTTCATA ATTATTGAA AAGAGGGTT TTGGGGTTT  
1751 GGGGTTTGG GG

FIGURE 12

1 CCCCCAAAACCCAAAAACCCAAAAACCCCTATAAAAAGAAAAATTGAGGTAGTTAGA 60  
 1 GGGGTTTGGGTTTGGGTTGGGATATTTTTCTTTTAACTCCATCAAATCT  
 a P Q N P K T P K P L \* K K K K L R \* F R -  
 b P K T P K P Q N P Y K K R K N C G S L E -  
 c P K P Q N P K T P I K K E K I E V V \* K -  
 61 AATAAAATATTATCCTGCACAAATGGAGATGGATATTGATTTGGATATAGAAAATT 120  
 61 TTATTTATAATAAGGGCGTGTACCTCTACCTATAACTAAACCTACTATATCTTTAA  
 a N K I L F P H K W R W I L I W M I . K I -  
 b I K Y Y S R T N G D G Y C F G C Y R K F -  
 c \* N I I P A Q M E M D I D L D D X E N L -  
 121 TACTTCCTAACATCAACAAGTATAGCAGCTTGAGTGACAAGAAAGGATGCAAA 180  
 121 ATGAAGGATTATGTAAGTTGTCATATCGTCGAGAACATCACTGTTCTTCTACGTTT  
 a Y F L I H S T S I A A L V V T R K D A K -  
 b T S \* Y I Q Q V \* Q L L \* Q E R M Q N -  
 c L P N T F N K Y S S S C S D K K G C K T -  
 181 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCAAAGTTGCAAAAATTAG 240  
 181 GTAACTTTAGACCGACGTTAGCGGAAGTAACTGATAAGCTTCAACGTTTGTAAATC  
 a H C N L A R N R L H C L F Q S C K N N -  
 b I E I W L E I A F I D Y S K V A K T I R -  
 c L K S G S K S P S L T I P K L Q K Q L E -  
 241 AGTTCTACTTCGGATGCAAATCTTATAACGATTCTTCTGAGAAAATTAGTTTAA 300  
 241 TCAAGATGAAGAGCCTACGTTAGAAATATTGCTAAGAAAGAACTTTAATCAAATT  
 a S S T S R M Q I F I T I L S C E N \* F -  
 b V L L E G C K S L \* R F F L E K I S F K -  
 c F Y F S D A N L Y N D S F L R K L V L K -  
 301 AAAGCCGAGAGCAAAGACTAGAAATTGAAACATTACTAATGTTAAATAAAATCAGGTA 360  
 301 TTTCGCCCTCGMTCTCATCTTAACCTTCTAATGATTACAAATTATTTAGTCCATT  
 a K A E S K E \* K L K H Y \* C L N K I R -  
 b K R R A K S R N C N I T N V \* I K S G N -  
 c S G E Q R V E I E T L L M F K \* N Q V M -  
 361 TGAGGATTATTCTATTTCAGATCACTCTTAAGGAGCATTATGGAGAAAATTACTAA 420  
 361 ACTCCTAACATAGATAAAATCTAGTAAGAATTCTCGTAATACCTCTTTAATGAATT  
 a C G L F Y F L D H F L R S I M E K I T -  
 b E D Y S I F \* I T S \* G A L W R K L L N -  
 c R I I L F F R S L L K E H Y G E N Y L I -  
 421 TACTAAAAGTAAACAGTTGATTATTCCTAGCCAACATGATGACTATATTAAATT 480  
 421 ATGATTTCCATTGTCAAACCTAACAAAGGGATCGGTTGTTACTACTCATATAATTAA  
 a Y \* K V N S L D Y F P S Q Q C C V Y \* I -  
 b T K R \* T V W I I S L A N N D E Y I K F -  
 c L K G K Q F G L F P \* P T M M S I L N S -

FIGURE 12 (cont.)

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAAGACAAACTCGCTAT  
 481 ----- 540  
 GTATACTCTTACTCGTTCTAGAGCTATGTAGTCTGAATGGTTCTGTTGAGCGATA  
  
 H M R M S Q R I S I H Q T Y Q R Q T R Y -  
 I C E C V K G S R Y I R L T K D K L A I -  
 Y E N E S K D L D T S D L P K T N S L -  
  
 AAAACGCAAGAAAAAGTTGATAATCGAACAGCGAGAAGAACTTATTGCATTTACTATTCG  
 541 ----- 600  
 TTTGCCCTCTTTCAAACTATTAGCTGTCGCTCTTGATAAACGTAATGATAAGC  
  
 K T Q E K V C - S N S R R T Y C I Y Y S -  
 K R K K K F D N R T A E E L I A F T I R -  
 N A R K S L I I E Q Q K N L L H L L F V -  
  
 TATGGGTTTATTACAATTGTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT  
 601 ----- 660  
 ATACCCAAAATAATGTTAACAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA  
  
 Y G F Y Y N C F R Y R R C T P E S C D N -  
 M G F I T I V L G I D G E L P S L E T I -  
 W V L L Q L F - V S T V N S R V L R Q L -  
  
 TGAAAAGCTGTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT  
 661 ----- 720  
 ACTTTTCGACAAATGTTGACTTCCTAGCGTCAAGACTTCAAGACTACACATACCGTA  
  
 C K S C L Q L K E S Q F C K F - C V C H -  
 E K A V Y N C R N R S S E S S D V Y A I -  
 K K L F T T E G I A V L K V L M C M P L -  
  
 TATTTGTGAATTAATCTCAAATATCTTATCTCAATTAAATGGATAGCTATAGAAACAAA  
 721 ----- 780  
 ATAAAACACTTAATTAGTTAGAGTTATAGAATAGAGTTAACCTATCGATATCTTGT  
  
 Y F V N - S Q I S Y L N L M D S Y R N K -  
 I L C I N L K Y L I S I - W I A I E T N -  
 F C E L I S N I L S Q F N G - L - K Q T -  
  
 CCAAATAAACCATGCAAGTTAATGAAATACGTTAAATCCTTGGACAAATGCACAC  
 781 ----- 840  
 GGTTTATGGTACGTTCAAATTACCTTATATGCAATTAGAAACCCGTGTTACGTGTC  
  
 P N K P C K F N G I Y V K S F G T N A H -  
 Q I N H A S L M E Y T L N P L G Q M H T -  
 K - T Y Q V - W N I R - I L W D K C T L -  
  
 TGAATTATATGGATTCTAAACCATAGATAACAGAAATGCTTAGAGACTGATTAGC  
 841 ----- 900  
 ACTTAAATATAACCTAAGAATTCTGATCTATGTCTTACGAAATCTCTGACTAAATCC  
  
 C : Y I G F L K H R Y T E C F R D C F S -  
 E F I L D S - S I D T Q N A L E T D L A -  
 N L Y A : L K A - I H R M L - R L I - L -  
  
 TTACAACAGATTACCTGTTGATTACTCTTGCTCATCTTATATCTTAAAGAAGCA  
 901 ----- 960  
 AATGTTGTCATAAGACAAACTAATGAGAACGAGTAGAGAAATATAGAAATTCTCGT  
  
 L Q Q I T C F D Y S C S S L I S L K E A -  
 Y N R L P V E I T L A H L L Y L - K K Q -  
 T T D Y L F C L L L L I S Y I F K R S R -  
  
 GCGAAATGAAAAGAACACTAAACAAAGAGATTCAAAATTGTTGATTCCTCTGTAACC  
 961 ----- 1020  
 CCGCTTACTTTCTGATTCTTCTAAAGTTAAACAACTAAGAACGATAGTGTAGGACTAAG  
  
 G E M K R R L K K E I S K F V D S S V T -  
 A K C K E D - R K R F Q N L L I L L - P -  
 R N E K K T K E R D F K I C C F F C N R -  
  
 GGAATTAAACAAAGAAATTAGCAACGAAAAAGAAGAGAGCTATCACAACTCTGATTG  
 1021 ----- 1080  
 CCTTAATTGTTCTCTTATAATCGTTGCTTTTCTCTCGATAGTGTAGGACTAAG  
  
 G I N N K N I S N E K E E E L S O S C F -  
 E L T T R I L A T K K K K S Y H N P D S -  
 N - O D E Y - O P K R R R A I T I L I L -

FIGURE 12 (cont.)

1081 T T A A G A T T C A A A A A T T C C A G G T A A G A G A G A T A C A T T C A T T A A T T C A T A T A T A G  
 a -  
 b A A T T C T A A G T T T A A G G T C C A T T C T C T A T G T A A G T A A T T T A A G T A T A A T A T C  
 c -  
 L K I S K I P G K R D T F I K I H I L - -  
 \* R F Q K F Q V R E I H S L K F I Y Y S -  
 K D F K N S R \* E R Y I H \* N S Y I I V -  
 T T T T C A T T C A C A C C T G T T A T T T C T T T A T C T T A A C A A T A T T T T G A T T A G C T G G A A  
 1140 a -  
 b A A A A G T A A A G T G T C G A C A A T A A A A G A A A A T A G A A T T G T T A T A A A A A C T A A T C G A C C T T  
 c -  
 F F I S Q L L F S F I L T I F F D \* L E -  
 F S F H S C Y F L L S \* Q Y F L I S W K -  
 F H F T A V I F F Y L N N I F C L A G S -  
 G T A A A A G T A T C A A T A A G A G A A G C G C T A G A C T G A G G T A A C T T A G C T T A T T C A C A T T C A T  
 1200 a -  
 b C A T T T T C A T A G T T A T T C T C T C G C G A T C T G A C T C C A T T G A A T C G A A T A A G T G T A A G T A  
 c -  
 V K S I K \* E K R \* T E V T \* L I H I H -  
 \* K V S N K R S A R L R \* L S L F T F I -  
 K K Y Q I R E A L D C G N L A Y S H S \* -  
 A G A T C G A C C T T C A T A T C C A A T A C G A T G A T A A G G A A A C A G C A G T C A T C C G T T T A A A A A  
 1260 a -  
 b T C T A G C T G G A A G T A T A A G G T T A T G C T A C T A T T C C T T T G T C G T C A G T A G G C A A A A T T T T T  
 c -  
 R S T F I Y P I R C \* G N S S H P F \* K -  
 D R P S Y I Q Y D D K E T A V I R F K N -  
 I D L H I S N T M I R K Q Q S S V L K I -  
 T A G T G C T A T G A G G A C T A A T T T T A G A C T C A A G G A A A T C G G A C G C G A A A T C T T A A T C A A A A A  
 1320 a -  
 b A T C A C G A T A C T C C T G A T T T A A A A T C T C A G T T C T T A C C T C G G C T T T A G A A T T A G T T T T T  
 c -  
 \* C Y E D \* I F R V K K W S R N L N Q K -  
 S A M R T K F L E S R N G A E I L I K K -  
 V L C G L N F \* S Q E M E P K S \* S K R -  
 G A A T T G C G T C G A T A T T G C A A A A G A A T C G A A C T C T A A T C T T C G T T A A T A A G T A T T A C C A  
 1380 a -  
 b C T T A C G C A G C T A T A C G T T T C T T A G C T T G A G T T T A G A A A G C A A T T A T T C A T A A T G G T  
 c -  
 E L R R Y C K R I E L \* I F R \* V L P -  
 N C V D I A K E S N S K S F V N K Y Y Q -  
 I A S I L Q K N R T L N L S L I S I T N -  
 A T C T T G A T T G A A G A G A T T G A C G A G G C A A C T G C A C A G A A G A T C A T T A A G A A A T A A A  
 1440 a -  
 b T A G A A C T A A C T T C T C T A A C T G C T C C G T T G A C C T G T C T T C T A G T A A T T C T T T A T T T  
 c -  
 I L I D C R D \* R G N C T E D H \* R N K -  
 S C L I E E I D E A T A Q K I I K E I K -  
 L D C L K R L T R Q L H R R S L K K \* S -  
 G T A A C T T T A T T A A T T A G A A T A A A C T A A T T A C T A A T A G A G A T C A C C G A T C T T C A A  
 1500 a -  
 b C A T T G A A A A T T A T C T C T T A T T G A T T T A T G A T T A T C T C T A G T C C T A G A A G T T  
 c -  
 V T F I N \* R I N \* I T N I E I S D L Q -  
 \* L L I R E \* T K L L I \* R S A I F N -  
 N F Y \* L E N K L N Y \* Y R D Q R S S I -  
 T T G A C G A A A A A A G C T G A A C T A A A G T T A G A C A A T A A A A A T C A A A C C T T G G T C A A A A T  
 1560 a -  
 b A A C T G C T T T A T T T C G A C T T C A A T C T G T T A T T T T A T G T T T G A C C A G T T T A  
 c -  
 L T K \* K L N \* S \* T I K N T N L G Q N -  
 C R N K S C T K V R Q \* K I Q T L V K I -  
 D E I K A E L K L D N K K Y K P W S K Y -  
 A T T G A G G A A G C C A A G A G C C A C T T A G C A A A G A A A A A T A A G G C A A T A A A A A T G A  
 1620 a -  
 b T A A C T C C T T C T T C T G G T C A A T C G T T T C T T T T A T C C C T T A T T T A T T T A C T  
 c -  
 I E E G K E D Q L A K E K I R O \* ! K C -  
 L R K E K K T S \* Q K K K \* G N K \* N E -  
 C G R K R R P V S K R K N K A I N K M S -

FIGURE 12 (cont.)

1681 GTACAGAAGTGAAGAAATAAAAGATTTATTTTTCAATAATTATTCAAAGAGGGCTT  
-----+-----+-----+-----+-----+-----+-----+-----+  
CATGCTTCACTTCTTATTTCTAAATAAAAAAGTTATTAAATAACTTTCTCCCCAA 1740

a V Q K C R N K R F I F F N N L L K R G V -  
b Y R S E E I K D L F F S I I Y C K E G F -  
c T E V K K \* K I Y F F Q \* F I E K R G F -

1741 TTGGGTTTTGGGGTTTGGGG  
-----+-----+-----+-----+-----+-----+-----+-----+  
AACCCAAAACCCCAAAACCC 1762

a L C F W G F G -  
b W G F G V L G -  
c G V L G F W -

# FIGURE 13

2 EVDLENOADNHGIIHSALKTCEEIKEAKTLYSWI0QKVICR0RN0SQSHYKDL 51  
 19 ELELEMQENQNDIQVRVK. .IDDPKQY..LVNVTAACLLQEGSYYQDK 62  
 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF. STGLMIELIDKCLVELL 100  
 63 DERRVIIITKALL ...EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107  
 101 SSSDVS0R0KL0CFCFG0LKG0NQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150  
 108 CVVHKNTQPFIEKYFNKA0LLPNDLLEVCEFA0VLYI 144  
 151 IGNELFRHLYTKYLIFORTSEGT1VQFCGNNVFDHLKVNDKF0KKQGGA 200  
 145 FDAT0EKF0NLY .....LDRILS0DIRKELTFRKCLQR0CVRSKF 181  
 201 ADM0NE PRCCSTCKVN0VNEKDHF0LN0N1VPN0WNNMKSRTRIFYCTHF 247  
 182 SEFNEYQLGKYCTES. QRKKTMFRYLSVTNKQWDQTKKK. .... 220  
 248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTN1FRFNRIKKLKDKVIEKI 297  
 221 RKENLLT0LQ0A0KES0D0SKRETG. ....DIMNVEDAIKALKPAVMK0I 264  
 298 AYML0VKDFNFNYYLTKSCPLPENWRERKQK1ENLINKTREEKSKYEE 347  
 265 AKR0NAMK. ....KHMKA0PKIPNSTLESKYLTFKD 294  
 348 LFSYTTDNKC0VTQFINEFFYNILPKDFLTGRNRK0FQKKVKKYVELNKHE 397  
 295 LIKFCHISEP. ....KERVYKILGKKYPKTEEEYKA0FGDSASAPFN.PE 338  
 398 LIKHNLL0E0KINTREISWMQVETS0AKHF0YFDHENIYVLWKL0R0WIFEDL 447  
 339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSN0LPYMAMLRNLSN.. 386  
 448 VVSL0RCFFYVTEQQKS0KTYYRKNI0WDVIMKMSIADLK0KETLAEVQE 497  
 387 .....ILKAGVSD. .... 394  
 498 KEVEEWK0SLGFAPGK0LRLIPK0TTFRPIMTFNKKIVNS0RKT0KLTNT 547  
 395 .....TTHS 398  
 548 KLLN0SHMLKTLK0R0MF0KDPFGFAVFN0YDDVMKKYEEFVCKW0QVGQPKL 597  
 399 IVINK. ....ICEPKAVENSKM 415  
 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTA0QILKR0NNIVID 647  
 416 F. PLQFFSAIEAVN. EA0TKGFKAKK. ....REN0NLKGQIEAVKE..VVE 457  
 648 SKNFRK0EMK0YFRQKF0QKIALEG0QYPTLFSVLENEQ0DNLNAKKT0LIVE 697  
 458 KTDEEKKDM. ....ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496  
 698 AK0RNYFKKDNL0LPV0VINICQ0NYINFNGKFYK0T0KGI0PQGLCVSSILSS 747  
 497 IAVWK0NLDEIKGHTA0FSDVSGSMSTSMSG0ACKYGSVRTCLECALVGL 546  
 748 FYYATLEESS0LGFLRDES0MN0PENPNVN0L0MRLTD0YLLITTQENN0AVLF1 797  
 547 MVK0RCEKSSFY1FSSPSS0CNKCYLEVDL. .... 576  
 798 EK0LIN0SRENGFKF0NMKK. LQTSFPLSPSKF0AKYGMDSV0E0Q0NIVQD0YCD 846  
 577 ... PGDEL0RPSM0KLL0QEKGKLG0GG. TDFPYECIDEWT0K0N0KTHVD 617  
 847 WIG0C0SID0MKT0L0MPN0INL0R0E0G0L0C0T0L0J0N0M0T0K0K0A0S0W0L0K0K0L0K0S0F0L0M 896  
 618 NIVIL0SDMMIAEGYSDINVRGSSIVNSI. ....K0K0Y0K0D0E0V0N0 653  
 897 NN0I0HYFRK0T0T0D0F0A0K0T0L0N0K0L0F0I0S0C0G0Y0K0M0C0A0E0Y0K0D0. HFK0K0N0L0M 945  
 654 PNIK0IF. .AVD0LEG0Y0G. ....K0C0L0N0L0G0D0E0F0N0E0N0N0Y0I0K0F0G0M 687  
 946 SSM0ID0L0EV0S0K0I0Y0S0V0T0R0A0F0K0Y0L0V0C0N0K0D0T0I0F0G0E0H0Y0P0D0F0L0S0T0L0K0H0F0I0E0 995  
 688 SDSI. ....LKF0I0S0A0Q0G0GA. .... .NM0V0E0 706  
 996 IFSTK0K0Y0F0N0R0V0C0 1008  
 707 VI..K0N0F0A0L0Q0K0G0 717

# FIGURE 14

132 LSTQKQYFFQDEWNQVRAMIGNEL..FRHLYTKYLIFQRTSE..GTLVQFC 178  
 1 MSRRNQ.. .KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI 43  
 179 GNNVFHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLLNNIN 228  
 44 KEEDLKLKFKNQDQDGNSGNDDDDEE.....NNSNKQELLRRVN 84  
 229 VPNWNNMKSRTTRIFYCTHENRNNQFFKKHEFVSNNNISAMDRAQTIFTN 278  
 85 ... .OIKQQVQLIKK..VGSKVEKDLNLNEDENKKN 114  
 279 IFRFNIRKKLDKVIKIAIMLEKVKDFNFNYYLTKSCPLPENWRERKQ 328  
 115 GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164  
 329 KIENLINKTREEKSYYEELFSYTTDNKCVTQFINE..FFYNILPKDFLTG 377  
 165 DTEKWFEISHDQK.. .NYVSIYANQKTSYCWLKDYFNK 200  
 378 RNRKQNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAXHFYY 427  
 201 NNYDHNLVNSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID.... 242  
 428 FDHENIYVLWKLRLWI..FEDLVVSLIRCFFYVTEQQKSYSKYYYYRKNI 475  
 243 VNFDNNLCLALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290  
 476 WDViMKMSIADLKKTETAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP 525  
 291 FAVVFSHR ..HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330  
 526 IMTFNKKIVNSDRKTTKLTNTKLLNShLMLKTLKMRMFKDPPFGFAVFNY 575  
 331 VYSFSTDLKLV..TNKVQDYFKFLQEFPRLTHSVSSQAIIPVSATNAVENL 378  
 576 DDVMKKYEEFVCKWKQVCGQPKLF.. .FATMDIEKCYDS..VNREK 615  
 379 NVLLKKVKH ..ANLNLVSIPTQFNFDYFVNLLQHLKLEFGLEPNILTQKQ 426  
 516 LSTFL ..KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK 657  
 427 LENLLLSIKOSKNLKFRLNFTYVAQETSRKQILKQATTIKNLKNNKNO 476  
 558 DYFRQKFQKIALEGQGYPTLFSVLEN EQNDLNAKKTLIVEAKQRYFK 705  
 477 EETPETKDET?SESTSGMKFDHLSLTTELEDFSVN.. .LQATQEIQY 520  
 706 KDNELQPVN: CQYNYINSNQKFKQTKGIPQGLCVSSILSSFYyatLEE 755  
 521 DSLHKLLIRSTNLKKFKLSSYKEMEKSXMDTFIDLKNI....YETLNN 564  
 756 SSSLGFLRDESMPNPENPNVNLMLRTDDYLLITTOENNNAVLIEKLINVSR 805  
 565 ..LKRCSYNISNPNGHISYELTN .. .KDSTFYKFKLTLNQE 600  
 806 ENGFKNMKKLQTSPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK 855  
 601 LOHAKYTFK.. QNEFQFNNVSAKIESSSLESLEDIDSICKSIASCKNLO 648  
 856 TLALMPNINLRIGILCTLNLMOT.. KKASMWLKK..KLKSFLMNNITH 901  
 649 NVNI.. .IASLLYPNNIQKNPFNKPNNLLFFKQFEQLKNLENVSINC 691  
 902 YFRKTI.. TTEDFANKTLNKLFISSGGYKYMCAKEYKDHFKKNLAMSSH 948  
 692 ILDOHILNSISEFLEKNNKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL 741  
 949 IDLEVSKIISVT ..RAFFKYLVCNIKDT..IFGEEHY 982  
 742 NQVYINQQLEELTVSEVHKQVWENHKQAFYEPCLCEFIKESSQLQLIDF 791  
 983 PDFFLS TLXHPIEIFSTKKY IFNRVCMILKAKEAKLKSDOCQSLIQ 1028  
 792 DQNTVSDDSIIKILESISESKEYHHYRLNPSQSSSLIKSENEEIQELLK 840

### FIGURE 15

4 617	DIDLDDEINLLPNTFNKYSSSCSDKGCKTLKSGSKSPSLTIPK... NVKSAKIESSSLESLEDISLCKSIASCNQLQNVNIIASLLYPNNIQKNP	47 666
48	LOKQLEFYFSANLYNDSFLRLKLVLKSGEQRVE...IETLLM	86
667	FNKPNNLFFFQFEGLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL	716

## FIGURE 16

1 MEMDIDDDIENL . . . LPNTFNKYSSSCSDKKGCKTLKSGSKSPS.. 42  
| | | | | . . . | : | | . . . | | | . .  
491 TELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSHSGGAKKYGSVRTCLEC 540  
| : | | | : : | . . . | : | . . . | . . . |  
43 LTIPKLQKQ . . . LEFYFSDANLYNDSFLRKVLKSGEQRVEIETLL 85  
| : | | | : : | . . . | : | . . . | . . . |  
541 ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL 589

FIGURE 17

	Motif A	Motif B	Motif C	Motif D	Motif E
Consensus	h--hDn---h--h	h---+DP---SP	h-h---R	h-h---R	h-hGn-h
telomerase p123	GQPKLFFPATMDIEKCYDSYNTREKLSTFLKTTTQLL-100-RFYKQTKGIPQELCVSSILSSFYYATLEEESSLGFL	KQRNLHCTYDLYKRAFDSDIPHSVTLIOVLEIYKIN-	KYKYLGFQQ	KYKYLGFQQ	QDYCDWIGISI
Dong (LINE)	KQRNLHCTYDLYKRAFDSDIPHSVTLIOVLEIYKIN-	28-RQLAIKGIYQEDSLS?JWFCLALNPLSHQLHNDR	QAPTSBALCNAVULURRLLAGLA	QAPTSBALCNAVULURRLLAGLA	QAPTSBALCNAVULURRLLAGLA
a1 S. c. (group II)	FGGSNNPFPREVDLRKCFDTISHDLIIKELKRYISD-	26-HVPVGPRVCV	7-GIRYQYNVLPECEWKCSPAIEQSSMTKILEPFRKQN	7-GIRYQYNVLPECEWKCSPAIEQSSMTKILEPFRKQN	7-GIRYQYNVLPECEWKCSPAIEQSSMTKILEPFRKQN
HIV-RT	LKKKRSVTVLDVGDAYFSYPLDEDFRKYTAFTTIP-	68-RCYIREDGLEFQESSUSA?IVDLYVYDDLEFYSEPK			
L8543 .12 Y <sub>n</sub>	VLPPELYPKKFDVKSCYDSIPRMECMRILDAALKN-				

FIGURE 18

telomerase p43      LQK**Q**LEFYFSDANLYNDSFLRKLVLSGEQR**N**EIETLLM  
human La            ICH**Q**EY**Y**FGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK  
Xenopus LaA        ICE**Q**EY**Y**FGDHNLPRDKFLKQQI.LLDDGWVPLETMIK  
Drosophila La      ILR**Q**EY**Y**FGDANLNR**D**KFLREQIGKNEDGWVPLSVLVT  
S. c. Lhplp        CLK**Q**MEFYFSEFNFPYD**R**ELRTTAEK.NDGW**V**PISTIAT

### FIGURE 19

1 aacticattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa  
61 tagatttaat ttagaaagtta tcaattgaaa aatggaaattt gaaaacaact aagcacaata  
121 gccaaaagcc gaaaaattgtt ggfgggact tgaatttagag atgcaagaaa accaaatga  
181 tatataagggtt agggtaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcac  
241 atgttttgtt taggaaggta gtactacta agataaagat gaaagaagat atatcatcac  
301 taaagcacctt ctgaggtgg ctgagtcga tcctgagttc atctgctgtt tggcagttca  
361 catccgtaat gaacttaca tcagaactac cactaactac attgttagcat ttgttgtt  
421 ccacaagaat actcaaccat tcatcgaaaa gtactcaac aaagcagttt ttttgcttaa  
481 tgacttactg gaagtctgtt aatttgcata gtttctctat atttttgatg caactgaatt  
541 caaaaattttt tttttttttt ggtttttttt ttttttttttt ttttttttttt ttttttttttt  
601 taagtgtttt caaagatgct tcagaagcaa gttttctttaa ttcaacgaaat actaacttgg  
661 taagtattgtc actgaatctt aacgttggaa aacaatgttc cgtttacccctt cagtttccaa  
721 caagttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
781 ggcataaaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga  
841 agatgcaatc aaggctttaa aaccaggactt tttttttttt tttttttttt tttttttttt  
901 catgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
961 gaccccttcaag gatcttattttt tttttttttt tttttttttt tttttttttt tttttttttt  
1021 gatcccttggtaa aaaaatacc ctaagaccga agaggaatc aaagcagccctt tttttttttt  
1081 tgcattttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1141 aacatggggaa aatgtttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1201 ttcaagcaat taactcccat atatggccat tttttttttt tttttttttt tttttttttt  
1261 cggftttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1321 tgagaactttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1381 agttactaag ggattttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1441 agcagttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1501 aacccggaa gggaaattttt tttttttttt tttttttttt tttttttttt tttttttttt  
1561 cattttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1621 tgcaatctttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1681 gtatggttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1741 acgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1801 ttactttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
1861 agagaaaggaa aacatggggaa gggaaattttt tttttttttt tttttttttt tttttttttt  
1921 aaagaataaa actcacgtt acaatatgtt tttttttttt tttttttttt tttttttttt  
1981 atatccatgtt atcaatgtt aacatgtt aatgtt aatgtt aatgtt aatgtt aatgtt  
2041 tgaagttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
2101 taatctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
2161 aacatctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
2221 cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
2281 cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
2341 atttaagttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
2401 aaagaacaaa aaagattttttttt tttttttttt tttttttttt tttttttttt tttttttttt

## FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL  
VNVTAAACLQEGSYYQDKDERRIITKALLEVAESDPEFICQLAVYIRNELYIRTTN  
YIVAFCVVHKNTQPFIEKYFNKA VLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRLS  
QDIRKELTFRKCLQRCSVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK  
KKRKENLLTKLQAIKESEDKSRETGDIMNVEDAIAKALKPAVMKKIAKRQNAMKKHMK  
APKIPNSTLESKYLTFKDLIKFCHEPKERVYKILGKKYPKTEEEYKAAFGDSASAP  
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV  
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE  
AVKEVVEKTDEEKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG  
HTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ  
CNKCYLEVDLPGDELPSMQKLLQEKGKLGGGDFPYECIDEWTKNKTHVDNIVLSD  
MMIAEGYSDINVRGSSIIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI  
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

### FIGURE 21

1 tcaatactat taattaataa ataaaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa  
61 ctaaaaaaag ccataggcic ctataggcaa tgaaacaaat ctgatttg tattacaaa  
121 tctagaagt tacaaaagcc agatgagca ttataagacc tagtagtaat agatcaaaga  
181 ggaggatcic aagttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga  
241 tgcgtatgtat gaagaaaaca actcaaataa ataataagaa ttataagga gagtcatt  
301 gattaagtat caagttat tgataaaaaa agttggcti aaggtagaga aagattgaa  
361 ttgaacgaa gtgaaaaca aaaagaatgg acyttctgaa tagcaagtga aagaagagta  
421 attaagaacg attactgaag aataggtaa gtattaaat ttgtattt acatggacta  
481 ccagttatgat taaaatgaga gtggggcca tagaagacac agaagagaaa cagattatgaa  
541 tactgaaaaa tggttgaaa tatctatga ccaaaaaat tatgtatcaa ttacgc当地  
601 ctaaaagaca tcataatgtt ggtggctaa agattattt aataaaaaca attatgtat  
661 tcttaatgtt aacattaaaca gactagaaac tgaagccgaa ttctatgc当地 ttgtatgatt  
721 ttacaaaaca atcaaactt ctaataatc ttactagact. gttacatag acgttaattt  
781 tgataataat ctctgtatc tcgcattgct tagattttt ttatctatg aaagattca  
841 tattttgatataaagatctt cttatacaag aaattaat aattttgaga aaatttggta  
901 gctacttggaa actatctcg cagttgtctt ttctatcgc cacitacaag gcattcatt  
961 acaagttcti tgcaagcgt tctaataattt agttacatcc tcatacataa ttacgc当地  
1021 agatagctaa ttatgtat acctttctc tacagactt aaatttagttt acactaaca  
1081 agtccaagat tattttaaatg tcttataaga attccctcg tttactatg taagctatg  
1141 ggctatccc当地 gttatgtctt ctaacgc当地 agagaacctc aatgttttac ttaaaaagat  
1201 caagcatctt aatcttattt tagtttctat ccctacctaa ttcaattttt atttctactt  
1261 tggattttttaaataatgaa aattagatgaa ccaatataattt tgacaaaaca  
1321 aaagcttggaa aatcttactt tgagtataaa ataataaaa aatcttataat ttttaagatt  
1381 aaacttttac acctacgtt ctaagaaaac ctccagaaaaa cagatataa aacaagctac  
1441 aacaatcaaa aatcttataaacaataaaaaa tcaagaagaa actcttggaa ctaagatgaa  
1501 aactccaaggc gaaagcacaat gtttttgc当地 catcttctg aattaaccga  
1561 gcttgaagat ttacgc当地 accttgc当地 tacccaaagaa attttatgata gcttgc当地  
1621 acttttgc当地 agatcaacaa attttaagaa gttcaattttaaattt agttcaattttaaattt atgaaatgaa  
1681 aaagtagaaaa atggatataat tcaatgtatctt taagaatattt tatgaaatctt taaacaatctt  
1741 taaaagatgc tctgttataat tcaatgtatcc tcatggaaac atttctatg aactgacaaaa  
1801 taaaagattctt accttttataat tcaatgtatctt gacccatcaat taagaattttaaattt aacacgctaa  
1861 gttatctt aatggatataat tcaatgtatctt aaaatgtcaat aaatttgc当地  
1921 ttccic当地 gaaagcttgc当地 agatatttgc当地 tagtttgc当地 aatcttattt ctcttgc当地  
1981 aattttataat tcaatgtatctt ttatgc当地 cccatcaat tttagaaaaaa  
2041 tccttcaat aagccccatc ttcttttcaat gttatctt aatggatataat ttttttgc当地  
2101 aatgtatctt atcaactgtt ctcttgc当地 gcatatactt aatttctt aatggatataat  
2161 agaaaaaaaat aaaaatataat aagcatatctt ttgttggaaa tatttttataat tcaatgtatctt  
2221 tctgttattt acttataat ttttttataat tcaatgtatctt cctgttattt aatggatataat  
2281 cattatattt caatggatataat aatggatataat gttatgttgc当地 cataatgttgc当地  
2341 ccacaaagccaa aatggatataat aatggatataat gttatgttgc当地 atcaatgttgc当地  
2401 ctttgc当地 atagatttttgc当地 accaaaacac ttttttgc当地 gttatgttgc当地  
2461 agaatcttataat ttttttgc当地 agtcatatctt ttatgttgc当地 ttgttgc当地  
2521 ctttgc当地 aatggatataat aatggatataat gttatgttgc当地 atcaatgttgc当地  
2581 agggttttgc当地 gttatgttgc当地 acttataat cccatcttgc当地 ttgttgc当地  
2641 ctttgc当地 atcaatgttgc当地 gttatgttgc当地 ttttttgc当地  
2701 ttttttgc当地 ttttttgc当地 ttttttgc当地 ttttttgc当地  
2761 atatatttttgc当地 gttatgttgc当地 ttttttgc当地 aatggatataat  
2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK  
EEDLKLLKFKNQDQDGNSGNDDEENNSNKQQELLRRVNQIKQQVQLIKVGSKVEK  
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR  
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNYDHLNVSINRLETEAE  
FYAFDDFSQTIKLTNNSYQTVNIDVNFDDNNLCILALLRFLLSLERFNILNIRSSYTRN  
QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF  
STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSAVENLNVLKKVKHANLNL  
VSIPTQFNFDFYFVNQHLKLEFGLEPNILTQKLENLLSIKQSKNLKFLRLNFYTY  
VAQETSRKQILKQATTIKNLKNKNQEEETPETKDETPESTSGMKFFDHLSELTELED  
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSMDTFIDLKNIYETLNNLK  
RCSVNISNPNGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE  
SSSLESLEDIDSCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLFFKQFEQLK  
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPE  
LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSLQTLQLIDFDQNTVSD  
DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP  
LCLPTGTYYDYNNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKGCGHFNGLDEILTCFAL  
PNSRKIALPCLPGDLSHKAVIDHCIYLLTGELEYNNVLTFGYKIARNEDVNNSLFCHS  
ANVNVTLLGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK  
WVQRSSSSATAAQIKQLTEPVTKQFLHKLNISSSSFPYSKILPSSSIKKLTDLR  
EAIFPTNLVKIPQRLKVRJNLTQKLLKRHKRLNYVSILNSICPLEGTVLDLSHLSR  
QSPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLSLPLNGYLPFDSSLKKL  
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI  
VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRJIIPKKSNEFR  
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKJISPTQIADRIKE  
FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN  
TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV  
INIKKLAMGGFQKYNAKANRDKILA VSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN  
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF  
KDLSINVQTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSSNTS  
KFKDNILLRKEIQHLQAYIYIYIHVN

## FIGURE 24

*Oxytricha*  
*Euplotes*

LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT  
LCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

human  
tez1  
EST2  
p123

Motif 0

AKPLHWLMSVYVVELRSPPFYVTETTPQKNR  
IS2IEWLVLGKRSNAKMCLSDFEKRKQIIFAEPIYWLYNSPIIPILOQSFFYITSSSDLRNR  
LKDFRHLFISD---IWFTKHNFENLNQLAICFISHLPRQLIPKIIQTFFYCTEISSTVT-  
TREISWMQVET-SAKHPYYFDHEN-IYVLWKLRLWIFEDLVVSLIRCPFYVTEQQKSYSK  
.....\*\*\*

Motif 1

LFFYRKSVHSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRPIPCK--DGL  
TVYFRKDIKLLCRPPI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTP  
IVYFRHDTWNKLITPFIVEYFKTYLVEVVCRNHNSYTLS--NPNHSKMRRIIPKKSNNEF  
TYYYRKNIWDVIMKMSI-ADLKKEETLAEVQEKEVBEWKKS-LGFAPGKLRLIPKK--TTF  
...\*

Motif 2

RPIVNMDYVVGARTPRREKRAERLTSRVKALP-SVLNYERA  
RLITN-LRKRFLIKGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFKLEVYMKLLTF  
RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF  
RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKN-RMFKDPPGPAVFNYDDVMKKY  
\*\*

Motif 3 (A)

KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPPEPVIRKYATIHATS  
KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFPNTN  
EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLTTKLLSSDFWIMTAQILKRKN  
.\*.\*\*\*. .\*

FIGURE 26

ATTTATACTCATGAAAATCTTATTGAGTCATTCAAGACAAGCTGACATTGATCTACA  
GACCAACAGTACTTACAAAGAAAATTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT  
TCTAACTACGTGTTCGCACTACCAAATTCAAGAAAATAGCATTACCATGCCTTCTGG  
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATACCTGTTGACGGGCGAATT  
ATACAACAAACGTACTAACATTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG  
TCTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCCTGCTGGAAAAT  
GTTCCACAGTTGGTCGGTACATACGCATTGTTGATTATTGATCAATTATACAGTAAT  
TCAATTAAATGGGCAGTTTCACTCAAATCGTGGTAACAGATGTAACGAACCTCATCT  
GCCGCCAAATGGGTCACAGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA  
ACTTACAGAACCGAGTACAAATAAACATTCTACACAAGCTCAATATAAATTCCCTTTC  
TTTTTTCTTATAGCAAGATCCTCCTTCATCATCATCTATCAAAAGCTAACTGACTT  
GAGAGAAGCTATTTCACAAATTGGTTAAAATTCTCAGAGACTAAAGGTACGAAT  
TAATTGACGCTGCAAAGCTATTAAAGAGACATAAGCGTTGAATTACGTTCTATT  
GAATAGTATTGCCCACCATTGGAAGGGACCGTATTGGACTTGTGCAATTGAGTAGGCA  
ATCACCAAAGGAACGAGTCTGAAATTATCATTGTTATTACAGAAGTTATTACCCCA  
AGAAATGTTGGCTCAAAGAAAATAAGGAAAATTATCAAGAATCTAAATCTTTATT  
AAGTTACCCCTAAATGGCTATTACCATTTGATAGTTGTTGAAAAGTTAAGATTAAA  
GGATTTCGGTGGTTGTCATTCTGATATTGGTCACCAAGCACAATTGAAAACCTT  
GAATCAATTGGCGATTGTTCATTCCTGGCTATTAGACAACATAATTCCAAAATTAT  
ACAGACTTTTACTGCACCGAAATATCTTACAGTACAGAATTGTTACTTAGACA  
TGATACITGGAATAAACTTACACCCCTTTATCGTAGAATATTAAAGACGTACTTAGT  
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCACATTCAATCATAGCAA  
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAAGGATTATTGCCATCCATGCAG  
AGGGGCAGACGAAGAAGAATTACAATTATAAGGAGAATCACAAAATGCTATCCAGCC  
CACTAAAAAATTAGAATACCTAACAGAACAAAGGCCACTAGTTTACTAAATATA  
TTCTCCAACGAAATAGCTGACCGTACAAAGAATTAAAGCAGAGACTTTAAAGAAATT  
TAATAATGTCTTACCAAGAGCTTATTGATGTCAAATCTGCTATGATT  
CATACCAAGGATGGAATGTATGAGGAACTCAAGGATGCGCTAAAAATGAAAATGGTT  
TTTCGTTAGATCTCAATTCTCAATACCAATAAGGTGTATTGAAGTTATTAAATGT  
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT  
TCATTATCAAATCAGGATGTTATAAACGTTAGAGATGGAATATTAAAACAGCTT  
GTGGGTTGAAGATAAGTGTACATTAGAGAACAGTGGCTTTTCAAGGCTCTAGTTATC  
TGCTCCGATCGTTGATTGGTGTATGACGATCTCTGGAGTTTATAGCGAGTTAAAGC  
CAGTCCTAGCCAGGACACATTAATTAAAAGCTGGCTGACGATTTCTTATAATATCAAC  
AGACCAACAGCAAGTGTACATACCAAAAGCTGCCCCATGGGCGGATTCAAAAATATAA  
TGCAGAACGCAATAGAGAACAAATTAGCCGTAAAGCTCCCAATCAGATGATGATACGGT  
TATTCAATTGTCATGCAATGACATATTGTTAAAGAATTGGAAGTTGGAAACATTCAAG  
CACAATGAATAATTCCATATCGTTGAAATCTAGTAAAGGGATATTGAAAGTTAAT  
AGCGCTGTTAACACTAGAACATTAAACATTGACACAAATTAAATCAACAAA  
CACCCTCTCATGCAAATTGATCATGTTGAAAGAACATTGGAATGTTATAAATCTGC  
TTTAAGGATCTATCAATTAAATGTTACGCAAATATGCAATTTCATTGTTCTAACAG  
CATCATTGAAATGACAGTCAGCGGTTGTCATTACGAAATGTGATCCTTAATCGAGTA  
TGAGGTACGATTCAACCATATTGAATGGATTGGAAAGCCTATCTTCAAACACATCAA  
ATTAAAGATAATATCATTCTTGTAGAAAGGAAATTCAACACTTGCAAGC

**FIGURE 27**

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR  
AERLTSRVKALFSVLNYERA

**FIGURE 28**

GCCAAGTCCCTGCACTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGTC  
TTCTTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTCTACC  
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA  
GAGGGTGCAGCTGCGGGACGTGCGGAAGCAGAGGTCAAGGCAGCATGGGA  
AGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG  
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG  
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC  
GTGCTCAACTACGAGCGGGCGCG

## FIGURE 29

MTEHHTPKSRJLRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLSDVQTFSIFLHSTVVGF  
DSKPDEGVQFSSPKCSQSELIANVVQMFDESERRNLLMKGFSMNHEDFRAMHVNGVQNDLV  
STFPNYLISILESKNWQLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVKRK  
RTIETSITQNKSRKEVSWSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG  
LINAFAQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDEKILS  
YSLKPNQVFQFLRSILVRVFPKLIWGNQRIFEIILKDLTFLKLSRYESFLSYLMSNIKISEIEWLVL  
GKRSNAKMCLSDFEKRKQIFAEIFYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT  
SMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT  
LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMGRKKYFYRIDIKSCYDRIKQDLMFR  
IVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY  
WTKSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKGSVL  
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG  
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVIFIDITHNSKFNSCCNI  
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC  
LGMRDGLKPSFYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRJAD

### FIGURE 30

FIGURE 30 (cont.)

ATGgtacgtgcggctcgagacttcagaatattgacacatcagGCTTTTGTCTTGAATGAGAGATGGTTGAACCCCTTT  
TCAAATATCATCCATGCTCGAACAGCTAATATAACCAATTCAAGCTTACTGATCTTATCAAGCCGC  
TAAGACCAGTTTGCACAGGTGTTATTTTACATAGAAGAATAGCTGATTAAtgtcaatttcaattttatatacatccctt  
tattacttgttcttaacaatatttacaaatgtatgactgtcccccaaaagcaagcatactataggattcttagtaaagtaaaattaaatctgttatttagtttgattgacttgtctt  
atcccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccataaacggggatggtaaacattaaaagtaatacatacgaggctaattccctttcatttag  
aataaggaaagtggtttctataatgaataatgcccgcactaatgcaaaaaagacgaagattatctctaaacaagggggatagaacataccgaaggaaaagagagataat  
accagggttgttgaagaaaggcaaggataatttggacaacaagcttcgcagatgacaggctaaattttggatggcaattttggtaaaaggcccagggttatccatggccg  
gccttgtactgagacgaaaagaaactaaggatagtttgaataactaatagcttataatgtcttataaaggttttttccgtactcaatttgcattgggaaaagaaata  
gtgttaagccattttggattccgaaatagccaaattcttgttccctcaaagcggaaagtctaaagaacttataagcttgcaggctcaaaaactccctgatttaaggag  
gaatcttccaccgatgagaaatggatagcttacgcgtctgaggagaagcctaatttttgcaaaaaaagaaaatataitgggagacatctctgtatgcattggccg  
gagtagtccagcggatccgtatgtcaataacttctatgttgcactgtcgcttcgactctcgtagctcagcagtaagtgcaccaaggtaacc

### FIGURE 31

EST2 pep	FFYCTEISST	VITIVYFRHDT	WN---	KLIT	P----	FIVE	YFK-TYLVEN	40
Euplotes pep	FFYVTEQQKS	YSKTYYYRKN	IWDVI-MKMS	IAD---LKK	ETLA--EVQE			43
Trans of tetrahymen	-----KHKE	GSQIFYYRK	IWKLVSKLT	VKVRIQFSEK	NKQMKNNFYQ			44
Consensus	FFY.TE..K.	.S..YYRK.	IW...-KL..	-----F..K	.....V..			50
EST2 pep	NVCRNHNSY-	-----	TLSNFNHSKM	RILPKKSNN	FRM	IAIPCRG		79
Euplotes pep	KEVEEWKKSL	-----	-GFAPCKI	RILPKKITT	FRP	IMTFNKK		78
Trans of tetrahymen	KIQLEEEENLE	KVEEKLIPED	SFQKYPQCKE	RILPKKGS	FRP	IMTFLRK		92
Consensus	K...E.....	-----	...F..GKE	RILPKKGS	FRP	IMTF.RK		100
EST2 pep	ADEEEFTIYK	ENHKNAIOP	TKILEYR	RNTK	RPTSFTKIYS	PTQLADRIKE		129
Euplotes pep	IVNSDRKTTK	LTTNTKLNS	HLMLXTE	KN-----	RMFK	-DPFGFAVFN		120
Trans of tetrahymen	DKQKNIK	--LNLNQILMDS	QLVFRNLKD	-----	ML-G	-QKIGYSVFD		130
Consensus	.....K..K	LN.N..L..S	QL.L..EKN	-----	....	-..IG..VF.		150
EST2 pep	FKQRLLKKEN	NVL-----	-----	PELYFMKFD	VKSCYD			157
Euplotes pep	YD-DVMKHYE	EFVCKWKQVG	QKIEFFATMD	IEKCYD				155
Trans of tetrahymen	NK-QISEKFA	QFIEKWKNKG	RECIEYYVTL	-----				158
Consensus	.K...KMF..	.F..KWK..G	...E.F.T.D	...CYD				186

## FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK

S-2: RQH LKR VQL RDV SEA EVR QHR EA

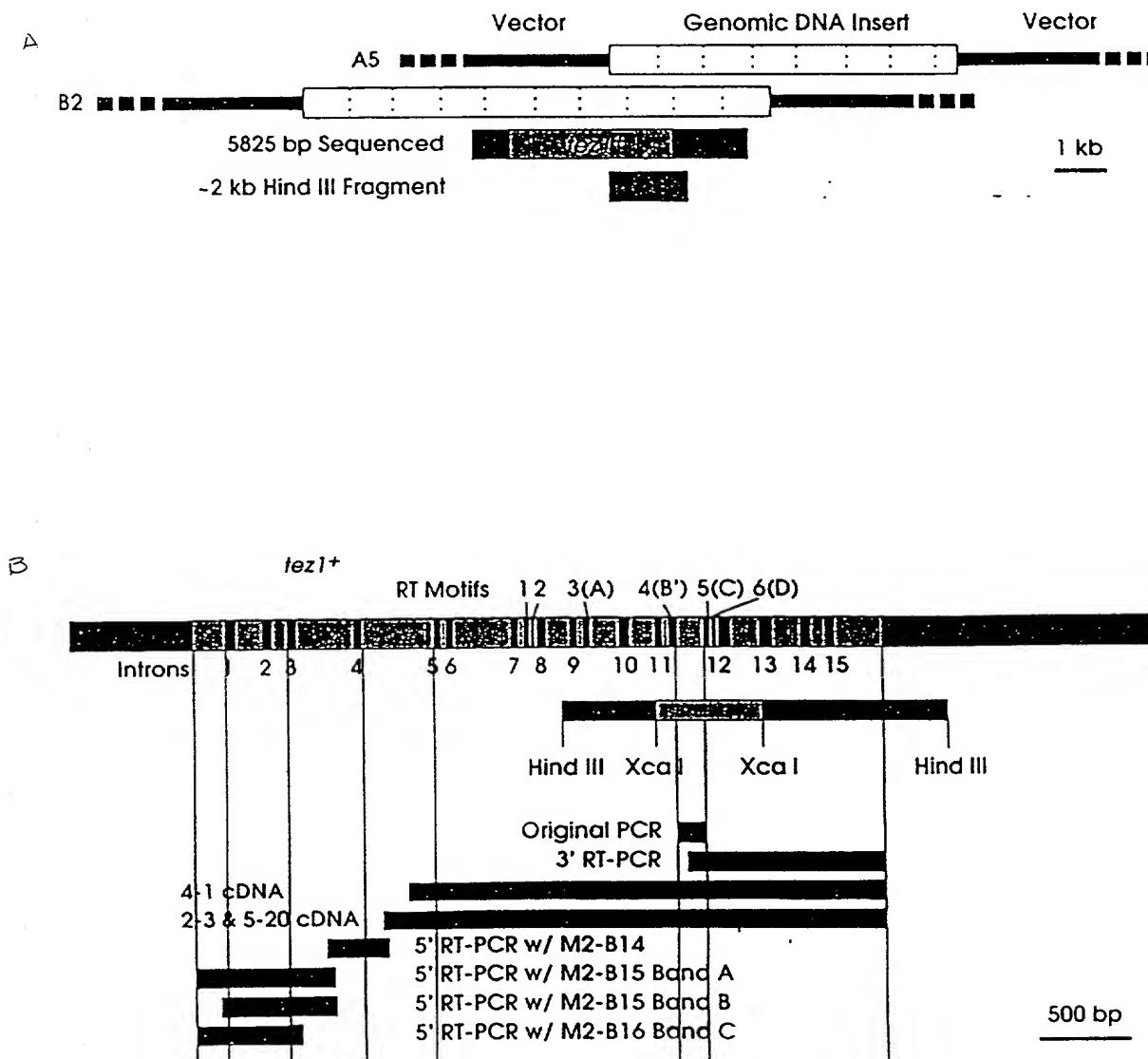
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q

A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS

A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIGURE 33



# FIGURE 34

## Poly 4

5' - t a a g c c t c g  
cag acc aaa gga att cca taa gg -3'  
Q T K G I P Q G

## 4 (B')

## 5 (C')

3' - D D Y L L I T  
ctg ctg atg gag gag tag tgg -5'  
a a a a a a a a  
t t t t t  
c c

## Poly 1

FIGURE 35

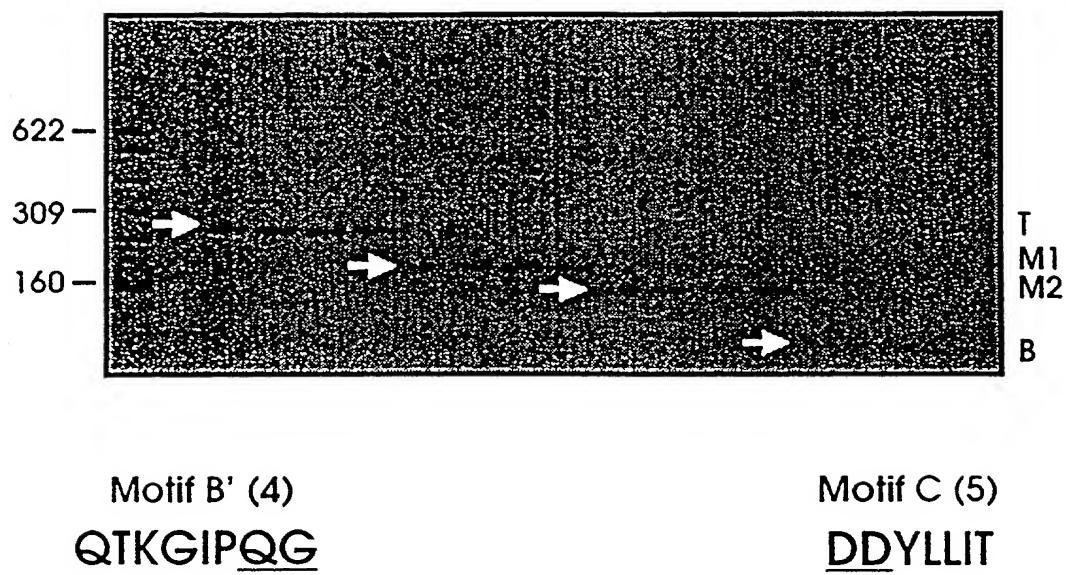


FIGURE 36

PCR Product M2 showed Reasonable Match  
with Other Telomerase Proteins

Ot	LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123	KGIPQGLCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRLTDYLLIT
Sp_M2	SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS

Q H K V G I P Q G  
caa Gaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4  
t t c  
t a a g c c t c g  
cag Gacc aaa gga att cca taa gg ----->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG  
tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA  
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc  
CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

<---- ctg ctg atg gag gag tag tgg  
a a a a a a a a  
t t t t t t  
c c

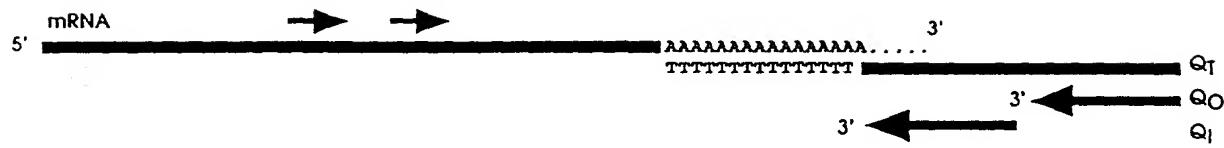
Poly 1

....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.

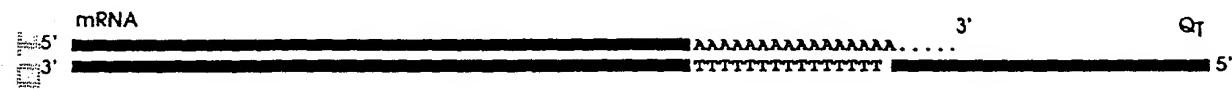
D D F L F I T

**FIGURE 37**

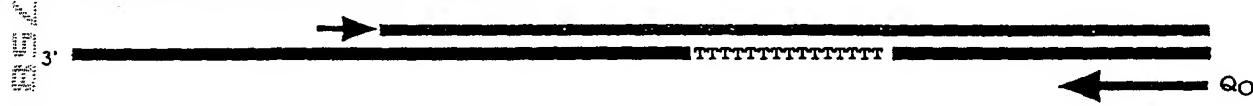
**3' RT PCR Strategy**



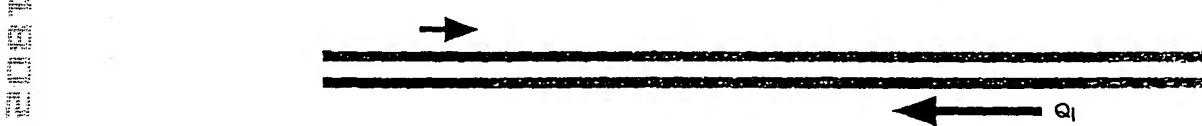
1. Synthesis of cDNA with QT Primer.



2. First Round PCR Using Outside Primer and QO Primer.



3. Second Round PCR Using Inside Primer and QI Primer.



4. Sequence Second Round PCR Products Using Inside Primer or QI Primer.



FIGURE 38

A

-Size Selected Libraries from P. Nurese

3 ~ 4 kb  
5 ~ 6 kb  
7 ~ 8 kb  
11 ~ 12 kb

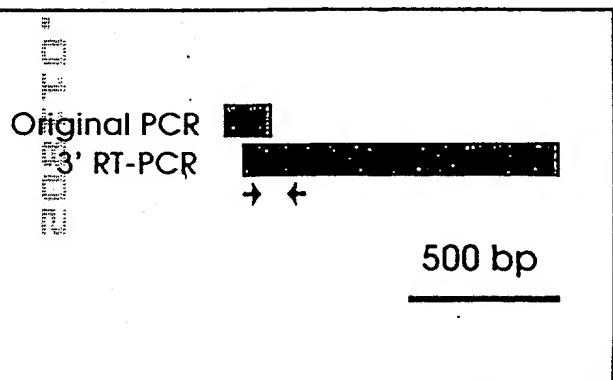
-Libraries from J.A. Wise

Sau 3a Partial Digest  
Hind III Partial Digest

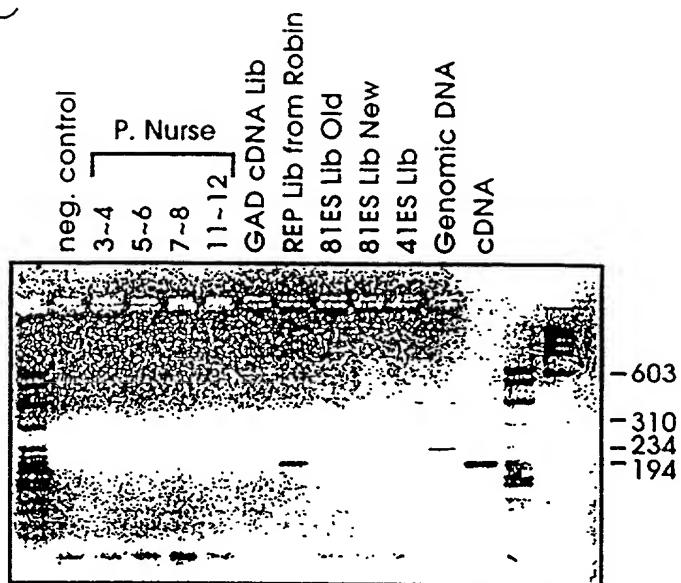
cDNA Libraries

GAD (Gal Activation Domain) Library  
REP Library from R. Allshire  
REP81ES Library (old)  
REP81ES Library (new)  
REP41ES Library

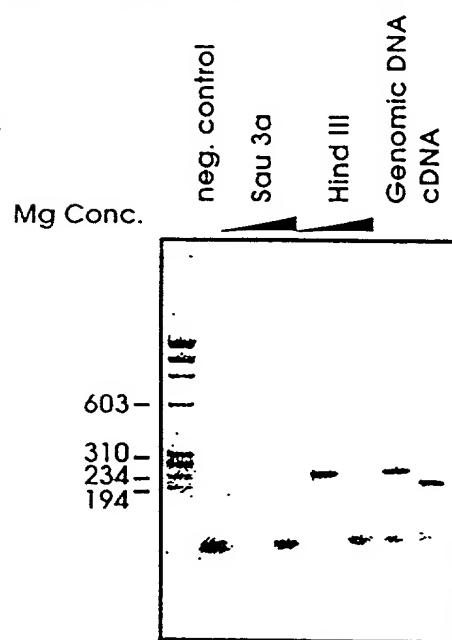
B.



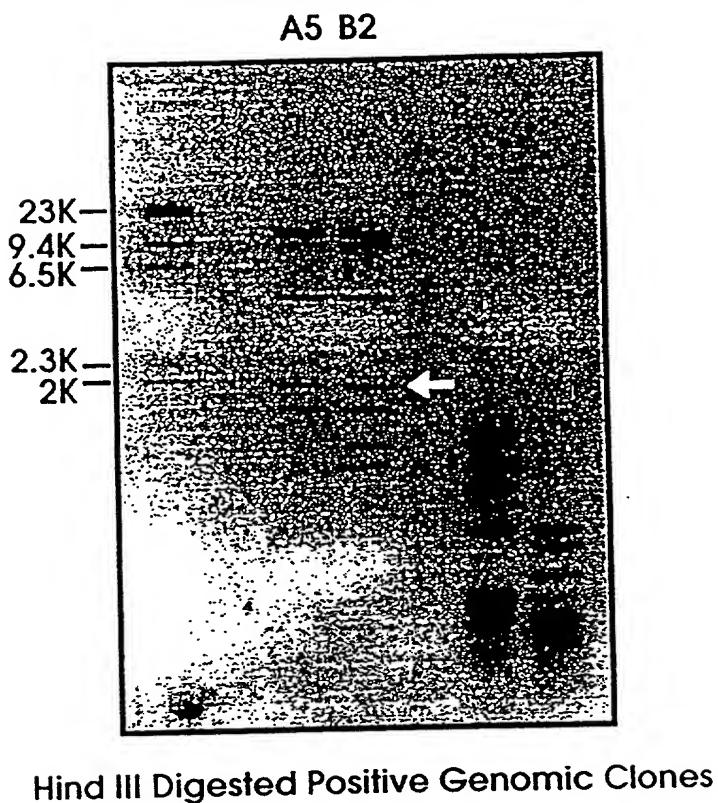
C



D

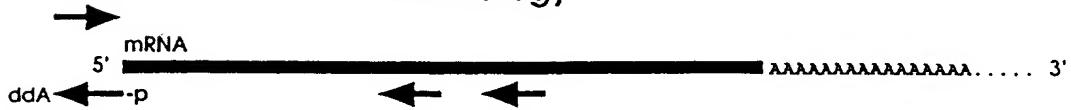


**FIGURE 39**

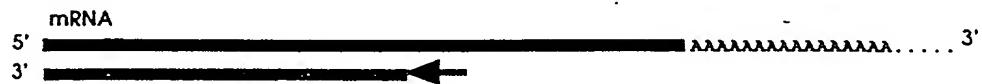


**FIGURE 40**

**5' RT PCR Strategy**



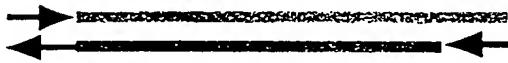
**1. Synthesis of cDNA with Specific Downstream Primer.**



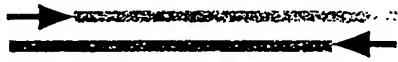
**2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.**



**3. First Round PCR**



**4. Second Round PCR**



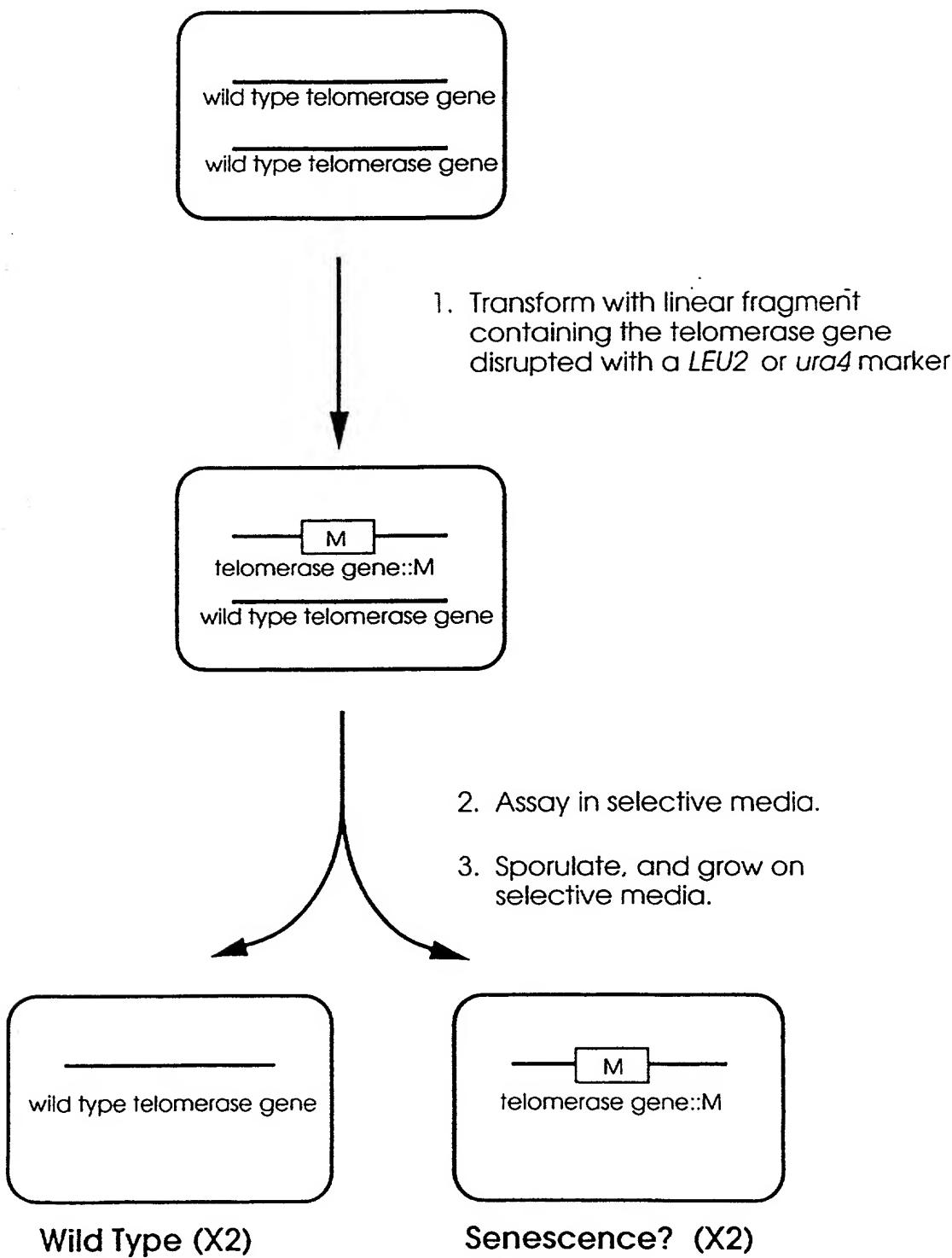
### FIGURE 41

## Alignment of RT Domains from Telomerase Catalytic Subunits.

## FIGURE 42

FIGURE 43

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

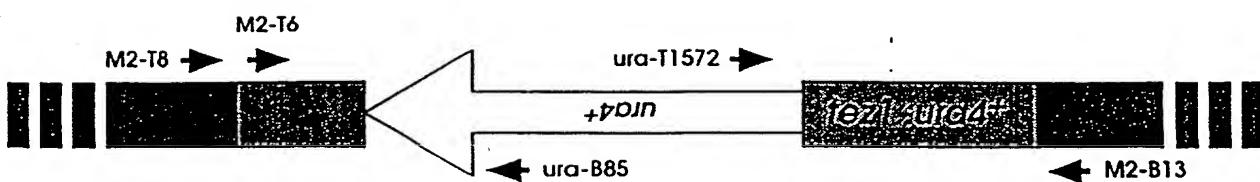
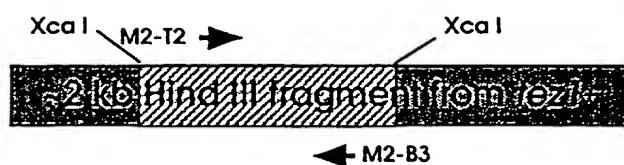
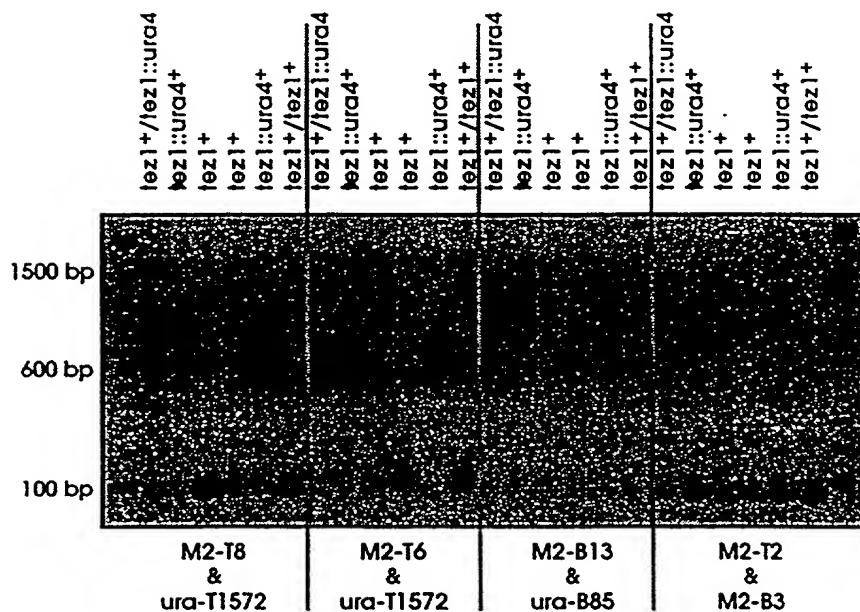


FIGURE 45

*Tez1* disruption causes progressive shortening of telomeres in *S. pombe*

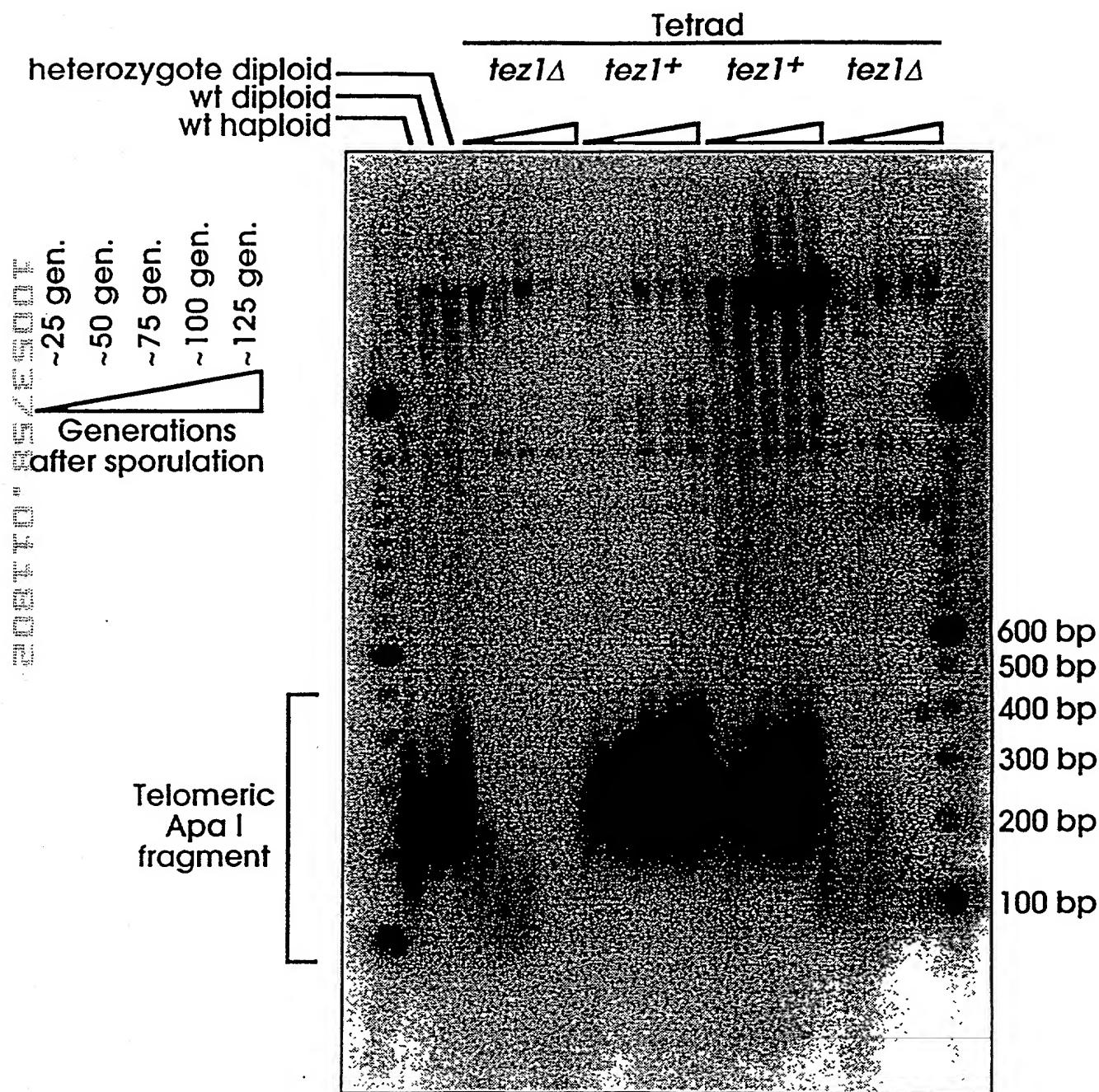


FIGURE 46

```

1 ggtaccgatttactttcccttcataagctaattgcctcgaacgcctaaatctggaaatattttacaaga 80
81 actcaataacaataccaagtcaaattccaatatgaagggttatttagtgcataatattctatttgcgtta 160
161 ccaagtataaggacaaaagaacaacttcctccccctaaagactttactttattaatttactttcaaatatattcg 240
241 gttcgcttactttatcggtactgtttagctgcacttgcacccgttctacccgtcatggatat 320
321 agctttggagtagctcacagaaatccatcaaattctctgatgagactatattgattcattacagtcgtgcatttc 400
401 ttaacatggagccttacactttagatgagtcacgtgcacatggagtattggatcatccaaacgttgcctgaaaag 480
481 gttgataattttgcaaatcatgtccttagtgggttaatccgcggaaagttttgatgcacacgtcttagcatg 560
561 attgagatattcaaaaattctatccactacaactcccttaacgcggtttatttctatttctattctatgttgc 640
641 ccaaataatgttatcatctgtttaggccttccgttactcctggaatcgtacctttactattccccataatga 720
721 ataatctaaatttagttcgcttataattgatagtagtagaaagattggtactcgtgtaatgttatttagttaaa 800
801 gatactttgcaaaacattttagctatcattatataaaaaaaatccatataattataatcaatattgcggtc 880
881 actatttatttaaacgttatgatcagtaggacacttgcataatataatgttatgcttaatggttactgtacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
   1 M    T    E    H    H    T    P    K    S    R    I    L    R    F    L    E    N    Q    Y    V    20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
   21 Y    L    C    T    L    N    D    Y    V    Q    L    V    L    R    G    S    P    A    S    S    40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
   41 Y    S    N    I    C    E    R    L    R    S    D    V    Q    T    S    F    S    I    F    L    60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
   61 H    S    T    V    V    G    F    D    S    K    P    D    E    G    V    Q    F    S    S    P    80

```

**FIGURE 46 (cont.)**

1199 AAA TGC TCA CAG TCA GAG gtatataaaaaatggggatcgatataatggcag	1272
81 K C S Q S E	86
1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA	1332
87 L I A N V V K Q M F D E S F E R R R N L	106
1333 CTG ATG AAA GGG TTT TCC ATG gtaaggattctaattgtgaaatattacctgcaattactgtttcaaagaga	1405
107 L M K G F S M	113
1406 ttgtatataaccgataaaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
114 N H E D F R A M H V N G V Q N	128
1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA	1529
129 D L V S T F P N Y L I S I L E S K N W Q	148
1530 CTT TTG TTA GAA AT gtaaaataccggtaagatgttgcgcacttgaacaagactgacaagtata T ATC GGC	1601
149 L L L E I	I G 155
1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC	1661
156 S D A M H Y L L S K G S I F E A L P N D	175
1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG	1721
176 N Y L Q I S G I P L F K N N V F E E T V	195
1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA	1781
196 S K K R K R T I E T S I T Q N K S A R K	215
1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT	1841
216 E V S W N S I S R F S I F Y R S S Y	235
1842 AAG AAG TTT AAG CAA G gtaactaatactgttatcccttcataactaatttttag AT CTA TAT TTT AAC	
1907	
236 K K F K Q D	L Y F N 245
1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG	1967
246 L H S I C D R N T V H M W L Q W I F P R	265
1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA	2027
266 Q F G L I N A F Q V K Q L H K V I P L V	285
2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA	2087
286 S Q S T V V P K R L L K V Y P L I E Q T	305
2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT	2147
306 A K R L H R I S L S K V Y N H Y C P Y I	325
2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG	2207
326 D T H D D E K I L S Y S L K P N Q V F A	345
2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA	2267
346 F L R S I L V R F P K L I W G N Q R I	365
2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaaatttattaccactaacgatttaccag AC CTC GAA ACT	2336
366 F E I I L K D	L E T 375

**FIGURE 46 (cont.)**

2337	TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396
376	F L K L S R Y E S F S L H Y L M S N I K	395
2397	gtaatatgc...aaatttttaccattaattaacaatcg ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396	I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525
406	K R S N A K M C L S D F E K R K Q I F A	425
2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585
426	E F I Y W L Y N S F I I P I L Q S F F Y	445
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645
446	I T E S S D L R N R T V Y F R K D I W K	465
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG	2705
466	L L C R P F I T S M K M E A F E K I N E	485
2706	gtat...aaagtat...ttgc...aaaagctaatat...tcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486	N N V R M D T Q K T	495
2776	ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835
496	T L P P A V I R L L P K K N T F R L I T	515
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtat...at...ggcatcaatgtacttacttcaatctatta	2906
516	N L R K R F L I K	524
2907	ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967
525	M G S N K K M L V S T N Q T L R P V	542
2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027
543	A S I L K H L I N E E S S G I P F N L E	562
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat	3088
563	V Y M K L L T F K K D L L K H R M F G	581
3089	tataatgcgcattcctcattataat...tcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA	3155
582	R K K Y F V R I D I	591
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC	3215
592	K S C Y D R I K Q D L M F R I V K K K L	611
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275
612	K D P E F V I R K Y A T I H A T S D R A	631
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagttat...ttcatt...aaat...ttacaa	3343
632	T K N F V S E A F S Y F	643
3344	attcttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405
644	D M V P F E K V V Q L L S M K T	659
3406	TCA GAT ACT TTG TTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465
660	S D T L F V D F V D Y W T K S S S E I F	679
3466	AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtaat...ccatt...ttgaatt...taataaca	3532
680	K M L K E H L S G H I V K	692

**FIGURE 46 (cont.)**

3533	ctaatgaaactag	ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA	3593
693	I G N S Q Y L Q K V G I P Q G S	708	
3594	ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG	3653	
709	I L S S F L C H F Y M E D L I D E Y L S	728	
3654	TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA	3713	
729	F T K K G S V L L R V V D D F L F I T	748	
3714	GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgtgtcattcc	3777	
749	V N K K D A K K F L N L S L R G	764	
3778	taagttctaaccgttgaag	GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA	3840
765	F E K H N F S T S L E K T V	778	
3841	ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA	3900	
779	I N F E N S N G I I N N T F F N E S K K	798	
3901	H AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT	3960	
799	R M P F F G F S V N M R S L D T L L A C	818	
3961	CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG	4020	
819	P K I D E A L F N S T S V E L T K H M G	838	
4021	AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtactgaataatagctgacaaaataatcg	A TCG	4089
839	K S F F Y K I L R	S	848
4090	AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT	4149	
849	S L A S F A Q V F I D I T H N S K F N S	868	
4150	TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA	4209	
869	C C N I Y R L G Y S M C M R A Q A Y L K	888	
4210	AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtaacttatttaactaga	4274	
889	R M K D I F I P Q R M F I T D	903	
4275	aaagtcatataattaaaccttag	AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC	4339
904	L L N V I G R K I W K K L A	917	
4340	GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc	4401	
918	E I L G Y T S R R F L S S A E V K W	935	
4402	ggtctcgagacttcagcaatattgacacatcag	G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA	4468
936	L F C L G M R D G L K	946	
4469	CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT	4528	
947	P S F K Y H P C F E Q L I Y Q F Q S L T	966	
4529	GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA	4588	
967	D L I K P L R P V L R Q V L F L H R R I	986	
4589	GCT GAT TAA tgtcatttcaatttattatatacatccttattactggtgtcttaacaatattactaagtata	4665	
987	A D *	989	

**FIGURE 46 (cont.)**

# FIGURE 47

1  
GCCAAGTTCCCTGCACTGGCTG met ser val tyr val val glu leu leu  
ATG AGT GTG TAC GTC GTC GAG CTG CTC

10  
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg  
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

20  
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile  
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

30  
gly ile arg gln his leu lys arg val gln leu arg glu leu ser  
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

40  
glu ala glu val arg gln his arg glu ala arg pro ala leu leu  
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

50  
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro  
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

60  
ile val asn met asp tyr val val gly ala arg thr phe arg arg  
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

70  
glu lys ala glu arg leu thr ser arg val lys ala leu phe  
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

80  
100  
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly  
AGC GTG CTC AAC TAC GAG CGG GCG CGC CCC GGC CTC CTG GGC

90  
ala ser val leu gly leu asp asp ile his arg ala trp arg thr  
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

100  
110  
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr  
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCT GAG CTG TAC

120  
130  
140  
phe val lys val asp val thr gly ala tyr asp thr ile pro gln  
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

150  
160  
170  
phe val leu arg leu thr glu val ile ala ser ile ile lys pro gln asn  
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

180  
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn  
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

**FIGURE 47 (cont.)**

FIGURE 47 (cont.)

390

leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln  
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400

410

ala tyr arg phe his ala cys val leu gln leu pro phe his gln  
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420

gln val trp lys asn pro his phe ser cys ala ser ser leu thr  
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430

440

arg leu pro leu leu leu his pro glu ser gln glu arg arg asp  
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450

val ala gly gly gln gly arg arg pro ser ala leu arg gly  
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460

470

arg ala val ala val pro pro ser ile pro ala gln ala asp ser  
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480

thr pro cys his leu arg ala thr pro gly val thr gln asp ser  
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490

500

pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys  
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510

pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp  
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520

530

his pro gly leu met ala thr arg pro gln pro gly arg glu gln  
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540

thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly  
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550

560

arg gly gly pro his pro gly leu his arg trp glu ser glu ala  
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564

OP

TGA GTGAGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCAGCACACCTGCGTTTCACTCCCCAC

CTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTCACTCCCCAC

**FIGURE 47 (cont.)**

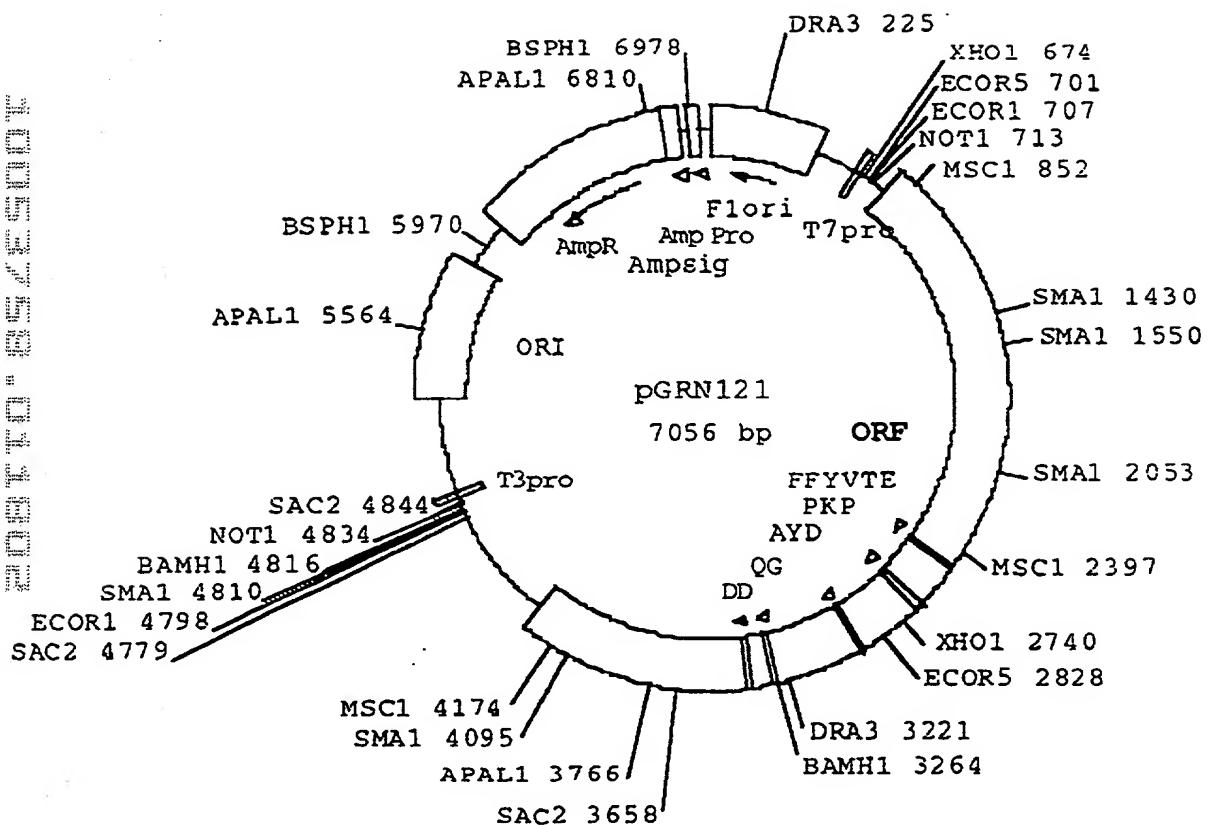
AGGCTGGCGTTCGGTCCACCCAGGGCCAGCTTTCTCACCA  
CCCCACATAGGAATAGTCCATCCCCAGATTGCCATTGTTCAC  
TTTGCCTTCCACCCCCACCATTCAAGTGAGACCTGAGAAGG  
AAGGACCTGGAGCTTG  
AATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGG  
ACCTGCACCTGGATGGGG  
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGAGTAAA  
AACTGAATATATGAGTT  
TTTCAGTTTGGAAAAAAAAAAAAAAA

## FIGURE 48

Motif -1	
Ep p123	...LVVSLIRCFYVTEQQKSYSKT...
Sp Tez1	...FIIPILQSFFYITESSDLRNRT...
Sc Est2	...LIPKIIQTFYCTEISSTVTIV...
Hs TCP1	...YVVELLRSFFYVTETTFQKNRL...
consensus	FFY TE
K	
Motif 0	p hhh K hR h R
Ep p123	...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1	...QKTTLPPAVIRLLPKKN--TFRLITNLRKRF...
Sc Est2	...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1	...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus	R PK RI
AF	
Motif A	h hDh GY h
Ep p123	...PKLFFATMDIEKYDSVNREKLSTFLK...
Sp Tez1	...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2	...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1	...PELYFVKVDVTGA YDTIPQDRLTEVIA...//...
consensus	F D YD
hPQG pS hh	
Motif B	
Ep p123	...NGKFYKQTKGIPQGLCVSSILSSFYA...
Sp Tez1	...GNSQYLQKVGVIPQGSILSSFLCHFYME...
Sc Est2	...EDKCYIREDGLFQGSSLSSAPIVDLVYD...
Hs TCP1	...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus	G QG S
Y	
Motif C	h F DDhhh
Ep p123	...PNVNLLMRLTDYLLITTQENN...
Sp Tez1	...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2	...SQDTLILKLAADDFLIISTDQQQ...
Hs TCP1	...RRDGLLLRLVDDFLLVTPHLTH...
consensus	DD L
Gh h cK	
Motif D	
Ep p123	...NVSRENGFKFNMKKL...
Sp Tez1	...LNLSLRGFEKHNFST...
Sc Est2	...KKLAMGGFQKYNAKA...
Hs TCP1	...LRTLVRGVPEYGCVV...
consensus	G

FIGURE 49

000537562 0142602



## FIGURE 50

1 GCAGCGCTGC GTCCGTGTC GCACGTGGGA AGCCCTGGCC CCGGCCACCC  
51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCCTC CCTGCTGC  
101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTCGTGC GGCGCCTGGG  
151 GCCCCAGGGC TGGCGGCTGG TGCAAGCGG GGACCCGGCG GCTTCCGCG  
201 CGNTGGTGGC CCANTGCNTG GTGTGCCTGC CCTGGGANGN ANGGCNGCCC  
251 CCCGCCGCC CTCCTCCG CCAGGTGTCC TGCTGAANG ANCTGGTGGC  
301 CCGAGTGCTG CANANGCTGT GCGANCACGG CGCGAANAAAC GTGCTGGCCT  
351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCG CGAGGCCTTC  
401 ACCACCAGCG TGCGCAGCTA CCTGCCAAC ACGGTGACCG ACGCACTGCG  
451 GGGGAGCGGG GCGTGGGGGC TGCTGCCTGC CGCGTGGC GACGACGTGC  
501 TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC  
551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACAGCTCG GCGCTGCNAC  
601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC  
651 CAACGGGCCT GGAACCATAAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG  
701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC  
751 GTGCCCAAG AGGCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC  
801 CCGTTGGCA GGGTCCCTGG GCCCCACCCGG GCAGGACGCC TGGACCGAGT  
851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC  
901 CTCTTGAG GGTGCCTCT CTGGCACGCC CCACTCCCAC CCATCCGTGG  
951 GCCGCCAGCA CCACGCCGGC CCCCCATCCA CATCGCGGCC ACCACGTCC  
1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCCTCTAC  
1051 TCCTCAGGCC ACAAGNACAC TGCGNCCTC CTTCCCTACTC AATATATCTG  
1101 AGGCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG  
1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCG GCCTGCCCA  
1201 GCGNTACTGG CAAATGCCGC CCCTGTTCT GGAGCTGCTT GGGAACACCG  
1251 CGCAGTGCC CTACGGGTG TTCCCTCAAGA CGCACTGCC GCTGCAGCT  
1301 GCGGTACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAACGC CCCAGGGCTC  
1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG  
1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGC  
1451 CTGCTGCCT CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG  
1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT  
1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG  
1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC  
1651 ACCGTCTGCC TGAGGAGATC CTGGCCAAGT CCCTGCACG GCTGATGAGT  
1701 GTGTACGTG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC  
1751 GTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTGTC TGGAGCAAGT  
1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGC  
1851 CTGTCGGAAAG CAGAGGTCAAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT  
1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG  
1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTCCGCAG AGAAAAGAGG  
2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA  
2051 CGAGCGGGCG CGGCCCGCCCG GCCTCTGGG CGCCTCTGTG CTGGGCGCTGG  
2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCCTGT GCGGGCCCAAG  
2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA  
2201 CGACACCACCCAGGACA GGCTCACCGA GGTCACTGCC AGCATCATCA  
2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC  
2351 AGACCTCCAG CGTACATGC GACAGTCGT GGCTCACCTG CAGGANAACA  
2401 GCCCGCTGAG GGATGCCGTC GTCACTGAGC AGAGCTCCTC CCTGAATGAG  
2451 GCCAGCAGTG GCCTCTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC  
2501 CGTGCACATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG  
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG  
2601 AACAAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TCGGTTGGT  
2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC  
2701 TCAGGACCCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACCTG  
2751 CGGAAGACAG TGGTGAACCTT CCCTGTAGAA GACGAGGCCG TGGGTGGCAC  
2801 GGCTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCCTGG TGCGGCCCTGC  
2851 TGCTGGATAC CGGACCCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC  
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG  
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGCTT CTTGCCGCTG AAGTGTACACA  
3001 GCCTGTTCT GGATTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC  
3051 ATCTACAAGA TCCTCCTGCT GCAGGGTAC AGGTTTCACG CATGTGTGCT  
3101 GCAGCTCCCA TTTCATCAGC AAGTTGGAA GAACCCCACA TTTTCCCTGC  
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG  
3201 AACGCAGGGGA TGTGCGTGGG GGCCAAGGGC GCGCCGGCC CTCTGCCCTC  
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCCTGCTC AAGCTGACTC  
3301 GACACCGTGT CACCTACGTG CCACCTCTGG GGTCACTCAG GACAGCCCAG  
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC  
3401 CGCAGCCAAC CGGCCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT  
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC  
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC  
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT  
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA  
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTCCCCA CAGGCTGGCG  
3701 CTCGGCTCCA CCCCCAGGGCC AGCTTTCCCT CACCAGGAGC CCGGCTTCCA  
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC  
3801 GCCCTGCCCT CCTTGCCCTT CCACCCCCACCATCCAGGTG GAGACCCTGA  
3851 GAAGGACCCCT GGGAGCTCTG GGAATTGGA GTGACCAAAG GTGTGCCCTG  
3901 TACACAGGGCG AGGACCCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT  
3951 GGGGGGAGGT GCTGTGGAG TAAAATACTG AATATATGAG TTTTCAGTT  
4001 TTGAAAAAAA AAAAAAAA AAAAAAAA

### FIGURE 51

GCAAGCGCTGCGTCCCTGCCTGGCACGTGGAAAGCCCTGGCCCCGGCACCCCCCGCGCTGCC  
 1 +-----+-----+-----+-----+-----+-----+-----+-----+  
 CGTGGCGACGCCAGGACGACGGTGCACCCCTGGGGACGGGGCGGTGGGGGCGCTACGG  
  
 A A I R P A A H V G S P C P G H P K D A -  
 Q R C V L L R T W E A L A P A T P A M P -  
 S A A S C C A R G K P W F R P P F R C R -  
  
 GCGGGCTCCCGCTGGCGAGCGGTGGCTGGCTGGCGAGCCACTAACGGGAGGGTGGCT  
 61 +-----+-----+-----+-----+-----+-----+-----+-----+  
 CGCGCGAGGGGGCGACGGCTGGCACGGAGGGACGAAGCGTGGTGATGGCGCTACAGGA  
  
 A R S P L F S R A L P A P Q P L P R G A -  
 R A P R C R A V R S L L R S H Y R E V L -  
 A L P A A E P C A P C C A A T T A R C C -  
  
 GCGGCTGGCCACGTTGGTGGGGCGCTGGGGCCCAAGGGCTGGCGCTGGTGACAGCGCG  
 121 +-----+-----+-----+-----+-----+-----+-----+-----+  
 CGCGACACGGTGCAGGACGGCGCGACCCCGGGGTCGGACCGCGACCACGTCGGCGCG  
  
 A A G H V R A A P G A P G I A A G A A R -  
 P L A T F V R R L G P Q G W R L V Q R G -  
 R W P R S C G A W G P R A C C G W C S A G -  
  
 GGACCGGGGGCTTTCGGCGCNAGGTGGTGGCCCANGGCNGTGGTGTGGCTGGCCCTGGGANGN  
 181 +-----+-----+-----+-----+-----+-----+-----+-----+  
 CCTGGGGCGCGAAAGGGCGCNACCAACGGGTNAACGNAACACACGGCACCGCACCGCTNCN  
  
 G P G G F P R ? G G P ? ? G V R A L G ? -  
 D P A A F R A ? V A ? C ? V C V P W ? ? -  
 T R R L S A R W W P ? A W C A C F G ? ? -  
  
 ANGGCGGCCCCCGCTGGCTTCTGGCTGGCCAGGTGGTGGTGGCTGAANGANCTGGTGCG  
 241 +-----+-----+-----+-----+-----+-----+-----+-----+  
 TNCCCGCGGCGGGCGCGGGGGAGGAAGGGCGTCCACAGGACAGGACTTCTNGACCCACCG  
  
 ? A A P R R P L L P P C V L P E ? ? G G -  
 ? ? F P A A P S P R Q V S C L ? ? L V A -  
 G ? P P F P P P S A R C P A \* ? ? W W P -  
  
 CGAGGTGCTGCANANGCTGGGANCCCCGGGAANACGTGCTGGCCCTGGCTTGGCTTGG  
 301 +-----+-----+-----+-----+-----+-----+-----+-----+  
 GGCTCACGACGTNTACGACACGCTTGGCGCGGCTTNTTGACGGACUUAAGCCGAAGCG  
  
 P S A A ? A V R ? R R E ? R A G L R L R -  
 R V L ? ? I C ? R G A ? N V L A F G F A -  
 E C C ? ? C A ? A A R ? T C W P S A S R -  
  
 GCTGGACGGGGCCCGGGGGCCCCCGGAGGGCTTACACACAGGCGTGGCGAGCTA  
 361 +-----+-----+-----+-----+-----+-----+-----+-----+  
 CGACGACCTGGCGGG  
  
 A A G R G P R G P P R G I H H Q R A Q L -  
 L L D G A R G G F P E A F T T S V R S Y -  
 C W T G P A G A P F R E S P P A C A A T -

**FIGURE 51 (cont.)**

**FIGURE 51 (cont.)**

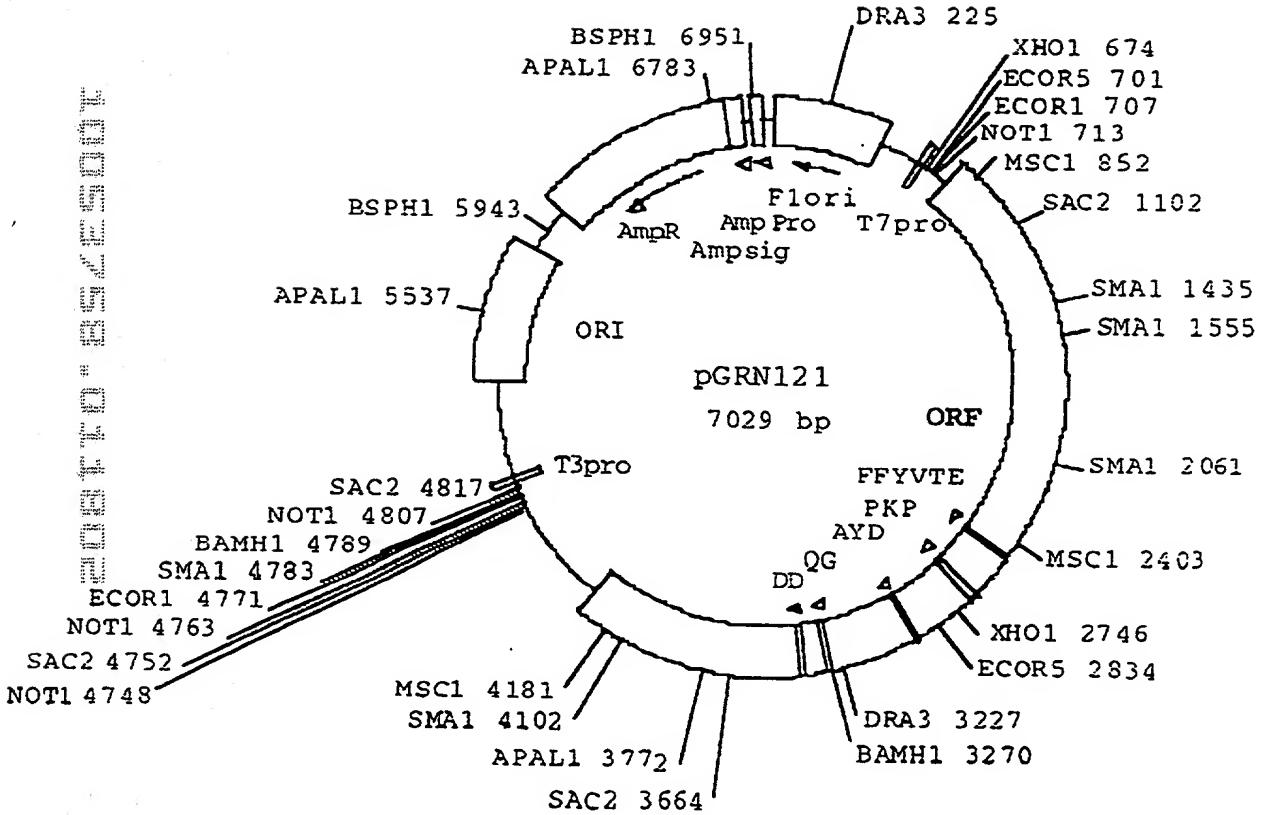
**FIGURE 51 (cont.)**

FIGURE 51 (cont.)

TCCCTCACTGCGCAGTGAAGTGTAQGTRGTCAGGCCTCACGGTCTTTCTTTATGTC  
 1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740  
 AGGAAGTGACCGACTACTCACACATGCCAGCAGCTGACGAGTCAGAAACAAAATACAGT  
  
 a S C T G \* V C T S S S C S C L S F M S -  
 b F A I A D E C V R R R A A Q V F L L C H -  
 c L H W I M S V Y V V E L L R S F F Y V T -  
  
 CGGAGACCAOFTTCAAAAGAACAGGCTCTTTCTACCGGAAGAGTGTCTGGAGCAAGT  
 1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1800  
 GCCTCTGGGAGCAAACTTTCTCTCGAGAAAAAGATGGCTCTCACASACCTCTCA  
  
 a R R P R F K R T G S F S T G R V S G A S -  
 b G D H V S K E Q A L F L P E E C L E Q V -  
 c E T T F Q K N R L F F Y R K S V W S K L -  
  
 TGCAAACCATTTGAATCAGACAGCACTTGAAGAGGGTGCAGCTGOGGGAGCTGTCGGAAAG  
 1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1860  
 ACGTTTGTAACTTGTCTGTGACTCTCTCCCACGTO3AQRCCTCTGACAGCCTTC  
  
 a C R A L E S D S T \* R G C S C G S C R K -  
 b A K H W N Q T A L E E C A A A C A V G S -  
 c Q S T G T R Q H L K R V Q L R E L S E A -  
  
 CAGAGGTCAGGCAAGCATGGCAACCCAGGCGGGCCCTGGTACAGTCAGACICCCCCTCA  
 1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920  
 GTCTTCACTTGGTGTACCCCTTGGTGGGGCGGGCGGACTCGAGCTGACGAGCTG  
  
 a Q R S G S I G K P G P P C \* R F D S A S -  
 b R G Q A A S C S O A R P A D V Q T P L H -  
 c E V R Q H R E A R P A L L T S R L R F I -  
  
 TCCCCCTAGCTGACGGGCTGCGGCCGATTGTGAAACATGGACTACGGTGTGGAGCCAGA  
 1921 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1980  
 AGGGGTGGGACTTCCCCGAGGGCGCTAACCTTGTCTGATGCAAGCACCCCTGGTCIT  
  
 a S P S L T G C G R L \* T W T T S W E P E -  
 b P Q A \* R A A A D C E H G L R R G S Q N  
 c P K P D G L R P I V N M D Y V V G A R T  
  
 CGTTCGGAGAGAAAAGAGGGCCGAGCTCTCACCTGGAGGGTGAAGRCACTGTTCAAGG  
 1981 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2040  
 GCAAGGGTCTCTTCTCCCGGCTGAGAGTGGAGCTCCACTTGGTGAACAAGTGCC  
  
 a R S A E K R C P S V S P K G \* R H C S A -  
 b V P Q R K E G R A S H L E G E G T V Q R -  
 c F R R E K R A E R L T S R V K A L F S V -  
  
 TGCTCCTACTACCAUCGGGGGGGGGGGGGGGGGGCTCTGGGCGCCACTGTCTGGGCCCTGG  
 2041 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2100  
 ACGAGTTGAGTGTCTGGCGCGCGCGCGGGGGGGAGACGACGGACCGACCGACCG  
  
 a C S T T S G R G A P A S W A P L C W A W -  
 b A Q L R A G A A P R P F G R I C A G E P G -  
 c L N Y E R A R R P G L L G A S V L G I D -

**FIGURE 51 (cont.)**

FIGURE 52



## FIGURE 53

1

met

GCAGCGCTGCGTCCGTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

30

his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50

60

phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70

ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80

90

leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110

120

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

↑

130

tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

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FIGURE 53 (cont.)

140 150

trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

160

leu leu ala arg cys ala leu phe val val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170 180

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

190

thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200 210

leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220

val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230 240

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250

ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260 270

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

280

val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

**FIGURE 53 (cont.)**

290 300  
gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC  
  
310  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC  
  
320 330  
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC  
  
340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA  
  
350 360  
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG  
  
370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC  
  
380 390  
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC  
  
400  
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG  
  
410 420  
val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA  
  
430  
ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

FIGURE 53 (cont.)

440 450  
ala prc glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460  
leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480  
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490  
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510  
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520  
met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540  
gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550  
ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570  
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580  
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590 600  
ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

FIGURE 53 (cont.)

610

ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620

630

leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640

pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650

660

arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670

phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGC CCC GGC CTC CTG

680

690

gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700

thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCT GAG CTG

710

720

tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730

gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC AAA CCC CAG

740

750

asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760

his gly his val arg lys ala phe lys ser his val ser thr leu  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

**FIGURE 53 (cont.)**

770 780  
thr asp ieu gln pro tyr met arg gln phe val ala his leu gln  
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG  
  
790  
glu thr ser pro leu arg asp ala val val ile glu gln ser ser  
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC  
  
800 810  
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg  
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC  
  
820  
phe met cys his his ala val arg ile arg gly lys ser tyr val  
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC  
  
830 840  
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu  
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC  
  
850  
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly  
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG  
  
860 870  
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu  
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG  
  
880  
leu val thr pro his leu thr his ala lys thr phe leu arg thr  
TTG GTG ACA CCT CAC ACC CAC GCG AAA ACC TTC CTC AGG ACC  
  
890 900  
leu val arg gly val pro glu tyr gly cys val val asn leu arg  
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG  
  
910  
lys thr val val asn phe pro val glu asp glu ala leu gly gly  
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC  
  
920 930  
thr ala phe val gln met pro ala his gly leu phe pro trp cys  
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

FIGURE 53 (cont.)

940

gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950

ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn  
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

960

970

arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980

val leu arg leu lys cys his ser leu phe leu asp leu gln val  
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

990

1000

asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010

leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1020

1030

his gln gln val trp lys asn pro thr phe phe leu arg val ile  
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040

ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1050

1060

ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
GCA GGG ATG TCG CTG CGG GCC AAG GGC GCC GGC CCT CTG CCC

1070

ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1080

1090

leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

**FIGURE 53 (cont.)**

1100 1110  
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr  
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120  
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp  
CTG ACT GCC CTG GAG GCC GCA AAC CCG GCA CTG CCC TCA GAC

1130 1132  
phe lys thr ile leu asp OP  
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCAGAGCAGA  
CACCAAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGCGGCCACACCC  
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCTGCATGTCC  
GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC  
CAGCACACCTGCCGTCTTCACTCCCCACAGGCTGGCGCTGGCTCCACCCCCAGGGCCAG  
CTTTCYTCACCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT  
CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTGCCCTCCACCCCCACCATCCAGGTGGA  
GACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTA  
CACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAATTGGGGGAGGTGC  
TGTGGAGTAAAATACTGAATATGAGTTTCAGTTTGRAAAAAAAAAAAAAAA  
AAAAAAAAAA

**FIGURE 54**

